PROGESTERONE RECEPTOR-REGULATED GENE EXPRESSION AND METHODS RELATED THERETO

CROSS-REFERENCE TO RELATED APPLICATIONS

This application claims the benefit of priority under 35 U.S.C. § 119(e) from U.S. Provisional Application Serial No. 60/214,870, filed June 28, 2000, entitled "Surrogate Gene Markers for Two Different Progesterone Receptor Isoforms in Breast Cancer, and Their Use to Screen for Isoform-Selective Progestational Ligands". The entire disclosure of U.S. Provisional Application Serial No. 60/214,780 is incorporated herein by reference.

FIELD OF THE INVENTION

This invention generally relates to expression profiles of genes that are regulated by progesterone receptors, and particularly by progesterone receptor isoforms PR-A and PR-B, and to the use of such genes in methods for identifying progesterone receptor agonist and antagonist ligands, including progesterone receptor isoform-specific ligands and tissue-specific ligands. This invention also relates to methods for determining the profile of genes regulated by progesterone receptors in a tissue sample. In addition, pluralities of polynucleotides transcribed from genes that are regulated by progesterone receptors are disclosed, as are pluralities of antibodies that selectively bind to proteins encoded by such genes.

BACKGROUND OF THE INVENTION

Progesterone is a natural reproductive hormone that targets the breast, uterus, ovaries, brain, bone, blood vessels, immune system, etc. Progestational agents are widely used for oral contraception, menopausal hormone replacement therapy, and cancer treatments. *Antiprogestins*, which are synthetic ligands that antagonize the actions of progesterone, are in clinical trials for contraception, for induction of labor, and to treat endometriosis, breast cancers and meningiomas. The actions of progesterone are varied and tissue-specific. Even in the normal breast it can have diverse effects: depending on the physiological state of the woman, progesterone can be proliferative, antiproliferative, or differentiative. Additionally, progesterone promotes the development of breast cancers and accelerates the growth of established breast cancers. For example, when used for hormone

replacement therapy at menopause, *progestins*, which are synthetic progestational agents, increase the risk of breast cancer. Paradoxically, they are protective in the uterus and prevent endometrial cancers.

Progesterone, synthetic progestins, and antiprogestins all initially work through the same molecular pathway. These are low molecular weight, lipid soluble *"ligands"*. They enter target cells passively, and pass into the nucleus where they bind to *progesterone receptors (PRs)*. Ligand binding activates the PR proteins, which then dimerize, bind to DNA at the promoters of progesterone target genes, and either up- or down-regulate transcription of these genes.

There are two natural isoforms of PR, the A- and B-receptors, also referred to herein as PR-A and PR-B, respectively. The isoforms are derived from two distinct promoters in the single PR gene and are translated from separate translation initiation start sites. PR-B receptors are 933 amino acids in length, which is 164 amino acids longer at the N-terminus than PR-A, and contain a unique transcriptional activation function, AF-3 (Sartorius *et al.*, *Mol. Endocrinol.* 8, 1347-1360 (1994)). Downstream of the additional 164 amino acids of PR-B, the two PRs have the identical primary amino acid content. However, despite this close amino acid composition, the two receptors have dramatically different abilities to activate transcription of progestin-responsive promoters in experimental model systems (Sartorius *et al.*, *Mol. Endocrinol.* 8, 1347-1360 (1994); Meyer et al., *J. Biol. Chem.* 267, 10882-10887 (1992); Vegeto *et al.*, *Mol. Endocrinol.* 7, 1244-1255 (1993); Tung et al., *Mol. Endocrinol.* 7, 1256-1265 (1993); Sartorius et al., *J. Biol. Chem.* 268, 9262-9266 (1993)). Progestin agonist-liganded PR-B are stronger transactivators than PR-A, although there are cell-type and promoter-dependent exceptions. The antiprogestin RU486 has mixed agonist/antagonist activity on PR-B but not PR-A. Instead, agonist or antagonist-liganded PR-A can dominantly inhibit PR-B and other members of the steroid receptor family, including estrogen receptors (ERs). Thus, PR-A are more likely to be transcriptional repressors than PR-B. (Hovland et al., *J Biol Chem* 273, 5455-60 (1998); Vegeto *et al.*, *Mol. Endocrinol.* 7, 1244-1255 (1993); McDonnell et al., *J. Biol. Chem.* 269, 11945-11949 (1994)).

Indirect data suggest that the two PR isoforms have physiologically different functions. They are unequally expressed in different tissues and physiological states. For instance, increasing ratios of PR-A to PR-B in the chick oviduct in late winter, or in aged, nonlaying hens, resulted in measurable decreases in PR functional activity (Boyd-Leinen et al., *Endocrinology* 111, 30-36 (1982); Spelsberg et al., *Endocrinology* 107, 1234-44 (1980)). There are stage-specific and region-specific variations in the PR-A:PR-B ratio in the developing rat brain (Kato et al., *J Steroid Biochem Mol Biol* 47, 173-82 (1993)) and studies in primates show that PR-B predominates in the estrogen treated hypothalamus, while expression of the PR-A isoform predominates in the pituitary (Baez *et al.*, *J Biol Chem* 262, 6582-8 (1987); Bethea et al., *Endocrinology* 139, 677-87 (1998)). In the human endometrium, absolute levels and the ratio of PR-A to PR-B vary extensively during the menstrual cycle (Mote et al., *Hum Reprod* 15 Suppl 3, 48-56 (2000); Mote et al., *J Clin Endocrinol Metab* 84, 2963-71 (1999); Mangal et al., *J Steroid Biochem Mol Biol* 63, 195-202 (1997); Feil et al., *Endocrinology* 123, 2506-2513 (1988)). In addition, uncontrolled, or over-expressed PR-B levels are associated with a highly malignant phenotype in endometrial, cervical and ovarian cancers (Farr *et al.*, *Mamm. Genome* 4, 577-584 (1993); Fujimoto et al., *J Steroid Biochem Mol Biol* 62, 449-54 (1997)).

In the normal breast, progesterone is both proliferative and differentiative [reviewed in\(Clarke et al., *Endocr. Rev.* 11, 266-301 (1990))]. Breast epithelium mitoses increase during the menstrual cycle and peak in the late luteal phase, coincident with high circulating levels of progesterone. Progesterone induces lobular-alveolar outgrowth during each menstrual cycle and during pregnancy induces further lobular-alveolar development in preparation for the terminal differentiative event of lactation. PR null mice exhibit incomplete mammary gland ductal branching and failure of lobulo-alveolar development, as well as failure to ovulate and to exhibit sexual behavior (Lydon *et al.*, *Genes Develop.* 9, 2266-2278 (1995)).

Little is known about cyclic changes in PR-A and PR-B in the normal human breast. However, in the mouse mammary gland, evidence supports a critical and unique role for each of the two PR isoforms. It has been reported that a 3:1 overexpression of PR-A over PR-B results in extensive mammary gland epithelial cell hyperplasia, excessive ductal branching,

and a disorganized basement membrane; all features associated with neoplasia (Shyamala et al., *Proc Natl Acad Sci U S A* 95, 696-701 (1998)). In contrast, when PR-B is overexpressed, ductal growth prematurely arrests and inappropriate lobulo-alveolar formation is observed (Shyamala et al., *Proc Natl Acad Sci U S A* 97, 3044-9 (2000)). However, when the PR-A isoform was selectively knocked out, leaving only PR-B, the mammary gland appeared to develop normally in response to estradiol and progesterone. In contrast, decidualization of the endometrium and the normal antiproliferative effect of progesterone in the uterus were absent (Mulac-Jericevic et al., *Science* 289, 1751-4 (2000)). Such data indicate that PR-A and PR-B have different tissue-specific effects.

In human breast cancers the presence of PR in estrogen receptor (ER) positive tumors indicates that responsiveness to endocrine therapies is likely, while absence of PR is associated with hormone resistance. thus, PR are routinely measured in breast cancers as a guide to treatment (Horwitz et al., *Recent Prog. Horm. Res.* 41, 249-316 (1985); Horwitz et al., *J Biol Chem* 253, 8185-91 (1978); McGuire, *Semin. Oncol.* 5, 428-433 (1978)). PR are also direct targets of second-line progestin therapies in patients whose tumors have developed antiestrogen resistance (Kimmick et al., *Cancer Treat Res* 94, 231-54 (1998); Howell *et al.*, *Recent Results Cancer Res* 152, 227-44 (1998)). Nothing is known, however, about the role of PR-A vs. PR-B in breast cancers. The PR-A to PR-B ratio was measured in 202 PR-positive human breast tumors (Graham *et al.*, *Cancer Res.* 55, 5063-5068 (1995)). The majority had PR-A to PR-B ratios greater than one, and 33% had 3.7 times or more PR-A than PR-B. The functional significance of this is unknown. In breast cancer cell lines, overexpression of PR-A results in marked changes in morphology and loss of adherent properties (McGowan et al., *Mol Endocrinol* 13, 1657-71 (1999)). Thus, overexpression of PR-A as seen in many breast tumors, may lead to suppression of PR-B, and may be associated with poor prognosis. However, there are no clinical data to support this conjecture.

Prior to the present invention, few, if any, endogenous genes differentially regulated by PR-A *vs.* PR-B were known in breast cancers or any other tissues. An excess of PR-A enhances the expression of SOX4 mRNA levels in breast cancer cells. Whether PR-B also regulates this gene is unknown. SOX4 induces DNA bending. PR-A enhance expression

of the mouse multiple drug resistance (mdr) 1b gene, important for development of drug resistance in tumors. Whether this gene is regulated endogenously only by PR-A is unknown. To the present inventors' knowledge, no data on PR-B specific gene regulation in breast cancers (or any tissues) has been published prior to the present invention. Although certain of the genes listed in Table 8 below were previously known to be progesterone regulated, the PR isoform specificity of this regulation was not known.

Knowledge of the unique sets of genes that are selectively regulated by each PR isoform would serve as a surrogate marker for the presence and function of PR-A *vs.* PR-B in various tissue types and in various disease states. Furthermore, knowledge of such genes and their promoters, would serve as a tool for screening PR ligands, and particularly, PR-A vs. PR-B selective ligands. However, defining which sets of genes are uniquely regulated by one or the other PR isoform in breast cancers was impossible in progesterone target tissues because both PR-A and PR-B receptors are simultaneously present in those tissues, and are simultaneously activated by progesterone treatment.

SUMMARY OF THE INVENTION

One embodiment of the present invention relates to a method to identify agonist ligands of progesterone receptors. The method includes the steps of: (a) contacting a progesterone receptor with a putative agonist ligand, wherein the progesterone receptor is selected from the group consisting of progesterone receptor A (PR-A) and progesterone receptor B (PR-B), under conditions wherein, in the absence of the putative agonist ligand, the progesterone receptor is not activated; (b) detecting expression of at least one gene that is regulated by the progesterone receptor when the progesterone receptor is activated; and, (c) comparing the expression of the at least one gene in the presence and in the absence of the putative agonist ligand, wherein detection of regulation of the expression of the at least one gene in the manner associated with activation of the progesterone receptor as set forth in (b) indicates that the putative agonist ligand is a progesterone receptor agonist.

In one aspect, detection of upregulation of expression of at least one gene chosen from a gene in Table 1, or detection of downregulation of at least one gene chosen from a gene in Table 2, in the presence of the putative agonist ligand, indicates that the putative

agonist ligand is a selective agonist of PR-A. In another aspect, detection of upregulation of expression of at least one gene chosen from a gene in Table 3, or detection of downregulation of at least one gene chosen from a gene in Table 4, in the presence of the putative agonist ligand, indicates that the putative agonist ligand is a selective agonist of PR-B.

Another embodiment of the present invention relates to a method to identify antagonists of progesterone receptors. This method includes the steps of: (a) contacting a progesterone receptor with a putative antagonist ligand, wherein the progesterone receptor is selected from the group consisting of progesterone receptor A (PR-A) and progesterone receptor B (PR-B), under conditions wherein, in the absence of the putative antagonist ligand, the progesterone receptor is activated; (b) detecting expression of at least one gene that is regulated by the progesterone receptor when the progesterone receptor is activated; and, (c) comparing the expression of the at least one gene in the presence and in the absence of the putative antagonist ligand, wherein detection of inhibition or reversal of the regulation of expression of the at least one gene as compared to the regulation of expression of the at least one gene in the manner associated with activation of the progesterone receptor as set forth in (b), indicates that the putative antagonist ligand is a progesterone receptor antagonist. The progesterone receptor can be activated by contacting the receptor with a compound that activates the receptor, the step of contacting being performed prior to, simultaneously with, or after the step of contacting of (a).

In one aspect of this embodiment, detection of inhibition of expression or downregulated expression of at least one gene chosen from a gene in Table 1 in the presence of the putative antagonist ligand as compared to the expression of the at least one gene in the presence of the compound that activates the progesterone receptor, or detection of inhibition of expression or upregulation of expression of at least one gene chosen from a gene in Table 2 in the presence of the putative antagonist ligand as compared to the expression of the at least one gene in the presence of the compound that activates the progesterone receptor, indicates that the putative antagonist ligand is a selective antagonist of PR-A. In another aspect, detection of inhibition of expression or downregulation of expression of at least one gene chosen from a gene in Table 3 in the presence of the putative antagonist ligand as

compared to the expression of the at least one gene in the presence of the compound that activates the progesterone receptor, or detection of inhibition of expression or upregulation of expression of at least one gene chosen from a gene in Table 4, in the presence of the putative antagonist ligand as compared to the expression of the at least one gene in the presence of the compound that activates the progesterone receptor, indicates that the putative antagonist ligand is a selective antagonist of PR-B.

In each of the above-described methods, the at least one gene is selected from the group consisting of: (i) at least one gene that is selectively upregulated by PR-A chosen from a gene in Table 1; (ii) at least one gene that is selectively downregulated by PR-A chosen from a gene in Table 2; (iii) at least one gene that is selectively upregulated by PR-B chosen from a gene in Table 3; (iv) at least one gene that is selectively downregulated by PR-B chosen from a gene in Table 4; (v) at least one gene that is upregulated or downregulated by both PR-A and PR-B chosen from a gene in Table 5; (vi) at least one gene that is reciprocally regulated by PR-A and PR-B chosen from a gene in Table 6; and, (vii) at least one gene that is regulated by one of the PR-A or the PR-B, wherein regulation of the gene is altered when the other of the PR-A or PR-B is expressed by the same cell, chosen from a gene in Table 7. In one embodiment, the method further includes a step of detecting expression of at least one gene chosen from the genes in Table 8.

In one aspect, step (b) includes detecting expression of: 11-beta-hydroxysteroid dehydrogenase type 2, tissue factor gene, PCI gene (plasminogen activator inhibitor 3), MAD-3 Ikβ-alpha, Niemann-Pick C disease (NPC1), platelet-type phosphofructokinase, phenylethanolamine n-methyltransferase (PNMT), transforming growth factor-beta 3 (TGF-beta3), Monocyte Chemotactic Protein 1, delta sleep inducing peptide (related to TSC-22), and estrogen receptor-related protein (hERRa1). In another aspect, step (b) includes detecting expression of: growth arrest-specific protein (gas6), tissue factor gene, NF-IL6-beta (C/EBPbeta), PCI gene (plasminogen activator inhibitor), Stat5A, calcium-binding protein S100P, MSX-2, lipocortin II (calpactin I), selenium-binding protein (hSBP), and bullous pemphigoid antigen (plakin family). In another aspect, step (b) includes detecting expression of phenylethanolamine n-methyltransferase (PNMT) adrenal medulla. In another aspect, step (b) includes detecting expression of proteasome-like subunit MECL-1. In

another aspect, step (b) includes detecting expression of: growth arrest-specific protein and tissue factor gene.

In each of the above-described methods, the progesterone receptor can be PR-A, PR-B or both PR-A and PR-B.

In one aspect of the above-described methods, the step (b) of detecting comprises detecting expression of at least five genes from any one or more of the Tables 1-7. In another aspect, the step (b) of detecting comprises detecting expression of at least ten genes from any one or more of the Tables 1-7. In yet another aspect, the step (b) of detecting comprises detecting expression of at least 15 genes from any one or more of the Tables 1-7.

In one aspect of the above-described methods, the progesterone receptor is expressed by a cell. In this aspect, the progesterone receptor is endogenously expressed by the cell or recombinantly expressed by the cell. In one embodiment, cell is part of a tissue from a test animal. In this embodiment, the step of contacting is performed by administration of the putative agonist ligand to the test animal or to the tissue of the test animal.

In another aspect of the above-described methods, expression of the at least one gene is detected by measuring amounts of transcripts of the at least one gene before and after contact of the progesterone receptor with the putative agonist ligand. In one aspect, expression of the at least one gene is detected by detecting hybridization of at least a portion of the at least one gene or a transcript thereof to a nucleic acid molecule comprising a portion of the at least one gene or a transcript thereof in a nucleic acid array. In another aspect, expression of the at least one gene is detected by measuring expression of a reporter gene that is operatively linked to at least the regulatory region of the at least one gene. In another aspect, expression of the at least one gene is detected by detecting the production of a protein encoded by the at least one gene.

In yet another aspect of the above-described methods, the putative agonist ligand is a product of rational drug design.

Yet another embodiment of the present invention relates to a method to identify isoform-specific agonists of progesterone receptors. This method includes the steps of: (a) contacting a progesterone receptor with a putative agonist ligand, wherein the progesterone receptor is selected from the group consisting of progesterone receptor A (PR-A) and

progesterone receptor B (PR-B), under conditions wherein in the absence of the putative agonist ligand, the progesterone receptor is not activated; (b) detecting expression of at least one gene that is regulated by the progesterone receptor when the progesterone receptor is activated; and, (c) comparing the expression of the at least one gene in the presence and in the absence of the putative agonist ligand, wherein detection of regulation of the expression of the at least one gene in the manner associated with activation of the progesterone receptor as set forth in (b)(i) but not (b)(ii), indicates that the putative agonist ligand is a PR-A-specific agonist, and wherein detection of regulation of the expression of the at least one gene in the manner associated with activation of the progesterone receptor as set forth in (b)(ii) but not(b)(i), indicates that the putative agonist ligand is a PR-B-specific agonist.

Another embodiment of the present invention relates to a method to identify isoform-specific antagonists of progesterone receptors. This method includes the steps of: (a) contacting a progesterone receptor with a putative antagonist ligand, wherein the progesterone receptor is selected from the group consisting of progesterone receptor A (PR-A) and progesterone receptor B (PR-B), under conditions wherein, in the absence of the putative antagonist ligand, the progesterone receptor is activated; (b) detecting expression of at least one gene that is regulated by the progesterone receptor when the progesterone receptor is activated; and, (c) comparing the expression of the at least one gene in the presence and in the absence of the putative antagonist ligand, wherein, in the presence of the putative antagonist ligand, detection of inhibition or reversal of the regulation of expression of the at least one gene as compared to the regulation of expression of the at least one gene in the manner associated with activation of the progesterone receptor as set forth in (b)(i) but not (b)(ii), indicates that the putative antagonist ligand is a PR-A-specific antagonist, and wherein, in the presence of the putative antagonist ligand, detection of inhibition or reversal of the regulation of expression of the at least one gene as compared to the regulation of the expression of the at least one gene in the manner associated with activation of the progesterone receptor as set forth in (b)(ii) but not (b)(i), indicates that the putative antagonist ligand is a PR-B-specific antagonist.

In each of the above-described methods of identifying a isoform-specific regulator of progesterone receptors, the progesterone receptor can include PR-A, PR-B, or both PR-A

and PR-B. The at least one gene is selected from the group consisting of: (i) at least one gene that is exclusively upregulated or downregulated by PR-A, chosen from a Table selected from the group consisting of Table 1 and Table 2; and, (b) at least one gene that is exclusively upregulated or downregulated by PR-B chosen from a Table selected from the group consisting of Table 3 and Table 4. In one aspect, the step (b) of detecting comprises detecting expression of at least five genes from any one or more of the Tables 1-4. In another aspect, the step (b) of detecting comprises detecting expression of at least ten genes from any one or more of the Tables 1-4. In yet another aspect, the step (b) of detecting comprises detecting expression of at least 15 genes from any one or more of the Tables 1-4.

Another embodiment of the present invention relates to a method to identify a tissue-specific agonist of a progesterone receptor. This embodiment includes the steps of: (a) providing an expression profile for at least one gene that is known to be regulated by a progesterone receptor in both a first and second tissue type when the progesterone receptor is activated, wherein the at least one gene is chosen from the genes in any one or more of the genes in Tables 1-7; (b) contacting a progesterone receptor expressed by a first tissue type with a putative agonist ligand, wherein the progesterone receptor is selected from the group consisting of progesterone receptor A (PR-A) and progesterone receptor B (PR-B), under conditions wherein, in the absence of the putative agonist ligand, the progesterone receptor is not activated; (c) contacting a progesterone receptor expressed by a second tissue type with the putative agonist ligand under conditions wherein, in the absence of the putative agonist ligand, the progesterone receptor is not activated, wherein the progesterone receptor is the same isoform as the progesterone receptor contacted in (b); (d) detecting expression of the at least one gene from (a); (e) comparing the expression of the at least one gene in the presence and in the absence of the putative agonist ligand in each of the first and second tissue types, wherein detection of regulation of the expression of the at least one gene in one of the first or second tissue types in the manner associated with activation of the progesterone receptor as set forth in the expression profile of (a), and detection of inhibition of regulation or no regulation of the at least one gene in the other of the first or second tissue types, as compared to the expression of the at least one gene associated with activation of the

progesterone receptor as set forth in the expression profile of (a), indicates that the putative agonist ligand is a tissue-specific progesterone receptor agonist.

Yet another embodiment relates to a method to identify a tissue-specific antagonist of a progesterone receptor. This method includes the steps of: (a) providing an expression profile for at least one gene that is known to be regulated by a progesterone receptor in both a first and second tissue type when the progesterone receptor is activated, wherein the at least one gene is chosen from the genes in any one or more of the genes in Tables 1-7; (b) contacting a progesterone receptor expressed by a first tissue type with a putative antagonist ligand, wherein the progesterone receptor is selected from the group consisting of progesterone receptor A (PR-A) and progesterone receptor B (PR-B), under conditions wherein, in the absence of the putative antagonist ligand, the progesterone receptor is activated; (c) contacting a progesterone receptor expressed by a second tissue type with the putative antagonist ligand, wherein the progesterone receptor is selected from the group consisting of progesterone receptor A (PR-A) and progesterone receptor B (PR-B), under conditions wherein, in the absence of the putative antagonist ligand, the progesterone receptor is activated; (d) detecting expression of the at least one gene from (a); and, (e) comparing the expression of the at least one gene in the presence and in the absence of the putative antagonist ligand in each of the first and second tissue types, wherein detection of regulation of the expression of the at least one gene in one of the first or second tissue types in the manner associated with activation of the progesterone receptor as set forth in the expression profile of (a) in the presence of the putative antagonist ligand, and detection of inhibition or reversal of regulation of expression of the at least one gene in the other of the first or second tissue types in the presence of the putative antagonist ligand, as compared to the expression of the at least one gene associated with activation of the progesterone receptor as set forth in the expression profile of (a), indicates that the putative antagonist ligand is a tissue-specific progesterone receptor antagonist.

Another embodiment of the present invention relates to a method to identify a tissue-specific agonist of a progesterone receptor. This method includes the steps of: (a) providing an expression profile for at least one gene that is known to be regulated by a progesterone receptor in a first tissue type but not a second tissue type when the progesterone receptor is

activated, wherein the at least one gene is chosen from the genes in any one or more of the genes in Tables 1-7; (b) contacting a progesterone receptor expressed by the first tissue type with a putative agonist ligand, wherein the progesterone receptor is selected from the group consisting of progesterone receptor A (PR-A) and progesterone receptor B (PR-B), under conditions wherein, in the absence of the putative agonist ligand, the progesterone receptor is not activated; (c) detecting expression of the at least one gene from (a); (d) comparing the expression of the at least one gene in the presence and in the absence of the putative agonist ligand in the first tissue type, wherein detection of regulation of the expression of the at least one gene in the first tissue type in the manner associated with activation of the progesterone receptor as set forth in the expression profile of (a) indicates that the putative agonist ligand is a tissue-specific progesterone receptor agonist for the first tissue type.

Yet another embodiment of the present invention relates to a method to identify a tissue-specific antagonist of a progesterone receptor. This method includes the steps of: (a) providing an expression profile for at least one gene that is known to be regulated by a progesterone receptor in a first but not in a second tissue type when the progesterone receptor is activated, wherein the at least one gene is chosen from the genes in any one or more of the genes in Tables 1-7; (b) contacting a progesterone receptor expressed by a first tissue type with a putative antagonist ligand, wherein the progesterone receptor is selected from the group consisting of progesterone receptor A (PR-A) and progesterone receptor B (PR-B), under conditions wherein, in the absence of the putative antagonist ligand, the progesterone receptor is activated; (c) detecting expression of the at least one gene from (a); and, (d) comparing the expression of the at least one gene in the presence and in the absence of the putative antagonist ligand in the first tissue type, wherein detection of inhibition or reversal of regulation of expression of the at least one gene in the first tissue type in the presence of the putative antagonist ligand, as compared to the expression of the at least one gene associated with activation of the progesterone receptor as set forth in the expression profile of (a), indicates that the putative antagonist ligand is a tissue-specific progesterone receptor antagonist of the first tissue type.

In each of the above-described methods to identify a tissue-specific regulator of a progesterone receptor, in one aspect, the first tissue type is breast, and wherein the at least

one gene is selected from the group consisting of: (i) at least one gene that is selectively upregulated by PR-A chosen from a gene in Table 1; (ii) at least one gene that is selectively downregulated by PR-A chosen from a gene in Table 2; (iii) at least one gene that is selectively upregulated by PR-B chosen from a gene in Table 3; (iv) at least one gene that is selectively downregulated by PR-B chosen from a gene in Table 4; (v) at least one gene that is upregulated or downregulated by both PR-A and PR-B chosen from a gene in Table 5; (vi) at least one gene that is reciprocally regulated by PR-A and PR-B chosen from a gene in Table 6; and, (vii) at least one gene that is regulated by one of the PR-A or the PR-B, wherein regulation of the gene is altered when the other of the PR-A or PR-B is expressed by the same cell, chosen from a gene in Table 7. In one aspect, the second tissue type is selected from the group consisting of breast, uterus, bone, cartilage, cardiovascular tissues, heart, lung, brain, meninges, pituitary, ovary, oocyte, corpus luteum, oviduct, fallopian tubes, T lymphocytes, B lymphocytes, thymocytes, salivary gland, placenta, skin, gut, pancreas, liver, testis, epididymis, bladder, urinary tract, eye, and teeth. In one aspect, the first tissue type is a non-malignant tissue and wherein the second tissue type is a malignant tissue from the same tissue source as the first tissue type. A preferred tissue source is breast tissue. In another aspect, the first tissue type is a normal tissue and wherein the second tissue type is a non-malignant, abnormal tissue.

In each of the above-described methods for identifying a tissue-specific regulator of a progesterone receptor, the expression profile of genes regulated by a progesterone receptor in the first or second tissue type can be provided by a method comprising: (a) providing a first cell of a selected tissue type that expresses a progesterone receptor A (PR-A) and not a progesterone receptor B (PR-B) and a second cell of the same tissue type that expresses PR-B and not PR-A; (b) stimulating the progesterone receptors in (a) by contacting the first and second cells with a progesterone receptor stimulatory ligand; (c) detecting expression of genes by the first and second cells in the presence of the stimulatory ligand and in the absence of the stimulatory ligand, wherein a difference in the expression of a gene in the presence of the stimulatory ligand as compared to in the absence of the stimulatory ligand, indicates that the gene is regulated by the progesterone receptor in the selected tissue type.

Another embodiment of the present invention relates to method to determine the profile of genes regulated by progesterone receptors in a breast tumor sample. This method includes the steps of: (a) obtaining from a patient a breast tumor sample; (b) detecting expression of at least one gene in the breast tumor sample that is regulated by a progesterone receptor when the progesterone receptor is activated; and, (c) producing a profile of genes for the tumor sample that are regulated selectively by PR-A, selectively by PR-B, or by both PR-A and PR-B. The at least one gene is selected from the group consisting of: (i) at least one gene that is selectively upregulated by PR-A chosen from a gene in Table 9; (ii) at least one gene that is selectively downregulated by PR-A chosen from a gene in Table 10; (iii) at least one gene that is selectively upregulated by PR-B chosen from a gene in Table 11; (iv) at least one gene that is selectively downregulated by PR-B chosen from a gene in Table 12; (v) at least one gene that is upregulated or downregulated by both PR-A and PR-B chosen from a gene in Table 13; (vi) at least one gene that is reciprocally regulated by PR-A and PR-B chosen from a gene in Table 14; and, (vii) at least one gene that is regulated by one of the PR-A or the PR-B, wherein regulation of the gene is altered when the other of the PR-A or PR-B is expressed by the same cell, chosen from a gene in Table 15.

Yet another embodiment of the present invention relates to a plurality of polynucleotides for the detection of the expression of genes regulated by progesterone receptors in breast tissue. The plurality of polynucleotides consists of polynucleotide probes that are complementary to RNA transcripts, or nucleotides derived therefrom, of genes that are regulated by progesterone receptors. The plurality of polynucleotides also comprises polynucleotide probes that are complementary to RNA transcripts, or nucleotides derived therefrom, of genes selected from the group consisting of: (a) at least one gene that is selectively upregulated by PR-A chosen from a gene in Table 1; (b) at least one gene that is selectively downregulated by PR-A chosen from a gene in Table 2; (c) at least one gene that is selectively upregulated by PR-B chosen from a gene in Table 3; (d) at least one gene that is selectively downregulated by PR-B chosen from a gene in Table 4; (e) at least one gene that is upregulated or downregulated by both PR-A and PR-B chosen from a gene in Table 5; (e) at least one gene that is reciprocally regulated by PR-A and PR-B chosen from a gene in Table 6; and, (f) at least one gene that is regulated by one of the PR-A or the PR-B,

wherein regulation of the gene is altered when the other of the PR-A or PR-B is expressed by the same cell, chosen from a gene in Table 7.

In one aspect, the polynucleotide probes are immobilized on a substrate. In another aspect, the polynucleotide probes are hybridizable array elements in a microarray. In another aspect, the polynucleotide probes are conjugated to detectable markers. In yet another aspect, the plurality of polynucleotides further comprises at least one polynucleotide probe that is complementary to RNA transcripts, or nucleotides derived therefrom, of at least one gene chosen from the genes in Table 8.

Another embodiment of the present invention relates to a plurality of antibodies, or antigen binding fragments thereof, for the detection of the expression of genes regulated by progesterone receptors in breast tissue. The plurality of antibodies, or antigen binding fragments thereof, consists of antibodies, or antigen binding fragments thereof, that selectively bind to proteins encoded by genes that are regulated by progesterone receptors. The plurality of antibodies, or antigen binding fragments thereof, also comprises antibodies, or antigen binding fragments thereof, that selectively bind to proteins encoded by genes selected from the group consisting of: (a) at least one gene that is selectively upregulated by PR-A chosen from a gene in Table 1; (b) at least one gene that is selectively downregulated by PR-A chosen from a gene in Table 2; (c) at least one gene that is selectively upregulated by PR-B chosen from a gene in Table 3; (d) at least one gene that is selectively downregulated by PR-B chosen from a gene in Table 4; (e) at least one gene that is upregulated or downregulated by both PR-A and PR-B chosen from a gene in Table 5; (e) at least one gene that is reciprocally regulated by PR-A and PR-B chosen from a gene in Table 6; and, (f) at least one gene that is regulated by one of the PR-A or the PR-B, wherein regulation of the gene is altered when the other of the PR-A or PR-B is expressed by the same cell, chosen from a gene in Table 7.

In one aspect, the plurality of antibodies, or antigen binding fragments thereof, further comprises at least one antibody, or an antigen binding fragment thereof, that selectively binds to a protein encoded by a gene chosen from the genes in Table 8.

Another embodiment of the present invention relates to a method to identify genes that are regulated by a progesterone receptor in two or more tissue types. This method

includes the steps of: (a) activating a progesterone receptor in two or more tissue types that express the progesterone receptor; (b) detecting expression of at least one gene the two or more tissue types, the at least one gene being chosen from a gene in any one or more of Tables 1-7, and, (c) identifying genes that are regulated by the progesterone receptor in each of the two or more tissue types. This method can further include the step of detecting whether the genes are regulated selectively by PR-A, selectively by PR-B, or by both PR-A and PR-B.

Another embodiment of the present invention relates to a method to regulate the expression of a gene selected from the group consisting of any one or more of the genes in Tables 1-7. The method includes administering to a cell that expresses a progesterone receptor a compound selected from the group consisting of: progesterone, a progestin, and an antiprogestin, wherein the compound is effective to regulate the expression of the gene. In one embodiment, the gene is selected from the group consisting of: growth arrest-specific protein (gas6), NF-IL6-beta (C/EBPbeta), calcium-binding protein S100P, MSX-2, selenium-binding protein (hSBP), and bullous pemphigoid antigen (plakin family). In another embodiment, the cell that expresses a progesterone receptor is in the breast tissue of a patient that has, or is at risk of developing, breast cancer.

DETAILED DESCRIPTION OF THE INVENTION

The present invention generally relates to the identification of a large number of genes that are regulated by progesterone receptors, and particularly, to the identification of *how* these genes are regulated by the progesterone receptor isoforms, PR-A and PR-B. Using the gene expression profiles disclosed herein, one can identify novel ligands of progesterone receptors (both progestin-like agonists and anti-progestin-like antagonists) that regulate progesterone receptors, including in an isoform-specific and/or tissue specific manner. In addition, these genes can be used to profile individuals that have been diagnosed with breast cancer to enhance the ability of the clinician to develop a prognosis and treatment protocols for the individual patient. The genes can also be used to profile the progesterone receptor regulated gene expression in tissue types other than breast tissue. Moreover, given the knowledge of these genes, one can produce novel combinations of polynucleotides and/or

antibodies and/or peptides for use in progestational drug screening assays or expression profiling of patient samples.

The present inventors have generated model systems to study PRs in breast cancer cells, that are unique to the present inventors' laboratory. In most target tissues, including the breast and uterus, PRs are induced by estradiol. Thus, one can only study progestin actions in the background of an estrogenized system. This makes it virtually impossible to dissect out responses that are due to progesterone, from those that are due to estrogens. Furthermore, all these target tissues contain both PR-A and PR-B. This makes it impossible to dissect out the effects of each PR isoform independently. The T47Dco breast cancer cells are unique to the present inventors' laboratory. They have retained PR and express both PR-A and PR-B at equal levels (Horwitz et al., *Cell* 28, 633-42 (1982)). However, the PRs in these cells are constitutively regulated without estrogens. In order to study differential gene regulation by the two PR isoforms independently, the present inventors constructed a model system in which a PR-negative subline (termed T47D-Y), was derived from T47Dco breast cancer cells. T47D-4 cells were then engineered to stably express either PR-B (termed T47D-4B) or PR-A (termed T47D-4A) at equal levels to each other and to the parental T47Dco cells (Sartorius *et al.*, *Cancer Res.* 54, 3668-3877 (1994)). The present inventors have now used these three new cell lines to analyze progesterone-responsive gene regulation via PR-B or PR-A (with PR negative T47D-Y cells serving as a control) using Affymetrix™ microarray HFL6800 gene expression chips and Atlas™ Human cDNA Expression Arrays. In addition to confirming the regulation of the few known progesterone-responsive genes, the present inventors have identified many genes not previously known to be regulated by PR. Importantly, the results described herein now allow discrimination of genes that are regulated uniquely by PR-B from genes that are uniquely regulated by PR-A. It was found that PR-B regulate more genes than PR-A in response to progesterone, but that a number of genes are uniquely regulated by PR-A. Many of these results have been confirmed by northern blot analysis or RT-PCR of the gene transcripts, or by western blot analyses of the protein products. The data presented herein demonstrate that the two PR isoforms do indeed have unique roles in gene regulation in breast cancer cells. Lastly, the present inventors have

observed that the expression levels of a subset of genes are modified by the presence of PR in a ligand-independent fashion.

Genes Regulated by Progesterone Receptors:

Of the more than 6000 human genes screened, the present inventors have identified multiple genes, the expression of which is regulated by progesterone receptors. The genes can be grouped into categories based on the regulation of expression of the genes by the progesterone receptor isoforms, PR-A and PR-B. More particularly, the genes have been grouped into the following main categories: (1) Genes that are selectively (i.e., exclusively or uniquely) upregulated by PR-A (Tables 1 and 9); (2) genes that are selectively downregulated by PR-A (Tables 2 and 10); (3) genes that are selectively upregulated by PR-B (Tables 3 and 11); (4) genes that are selectively downregulated by PR-B (Tables 4 and 12); (5) genes that are upregulated or downregulated in the same direction by both PR-A and PR-B (Tables 5 and 13); (6) genes that are reciprocally regulated by PR-A and PR-B (Tables 6 and 14); and (7) genes that are regulated by one of the isoforms, wherein such regulation is altered when the other isoform is present (e.g., the expression of the gene is either up- or downregulated in the presence of both receptors relative to the expression level of the gene in the presence of only one receptor) (Tables 7 and 15). In this last category, the gene is characterized in that the regulation of expression of the gene by one isoform is altered or suppressed by the presence of the other isoform. It is noted that genes in this last category can also fall within one of the other 6 categories. Tables 1-7 include all genes that were newly discovered to be regulated by progesterone receptors by the present inventors. Tables 9-15 include all of the genes from Tables 1-7, respectively, and additionally include the genes that were identified by the present inventors that had previously been identified to be regulated generally by progesterone. This particular subset of genes (i.e., previously known to be regulated by progesterone) is also set forth separately in Table 8. It is noted that even though the genes in Table 8 were known to be regulated by progesterone, the isoform specificity of these genes was not previously known. Therefore, the identification of the PR isoform regulation of the genes in Table 8 is novel. Other categories of the genes identified in the present invention are as follows: Table 16 is a list of genes identified in the present invention which were previously known to be involved in breast cancer or in the

development of mammary tissue. Table 17 is a list that categorizes the genes shown to be regulated by progesterone by the present inventors into functional categories based on GeneCard information as well as extensive literature reviews of each gene product. Table 18 (See Example 1) shows the cumulative results of the gene array analysis with regard to the PR-B-expressing cells described in the Examples. Table 19 (See Example 1) shows the cumulative results of the gene array analysis with regard to the PR-A-expressing cells described in the Examples.

Accordingly, in one embodiment of the present invention, the genes identified as being regulated by progesterone receptors by the present inventors can be used as endpoints or markers in a method to identify ligands that regulate progesterone receptor activity. According to the present invention, in general, the biological activity or biological action of a protein such as a progesterone receptor refers to any function(s) exhibited or performed by the protein that is ascribed to the naturally occurring form of the protein as measured or observed *in vivo* (i.e., in the natural physiological environment of the protein) or *in vitro* (i.e., under laboratory conditions). In particular, the biological activity of a progesterone receptor that is of interest herein includes the effect of the receptor, particularly when the receptor is activated, on the expression of the downstream genes identified in the present invention. According to the present invention, a "downstream gene" or "endpoint gene" is any gene, the expression of which is regulated (up or down) by a progesterone receptor (PR-A and/or PR-B). The expression of the gene is typically regulated by the progesterone receptor when it is activated, although the expression of the gene may be regulated by the progesterone receptor in the absence of a stimulatory compound (i.e., the regulation may be ligand independent, or constitutive). Pharmaceutical companies are keenly interested in screening their vast libraries of chemical compounds for ones that bind to (ligands), and either activate or inhibit, progesterone receptors. Selected sets of one, two, three, or more of the genes (up to the number equivalent to all of the genes) of this invention can be used as end-points for rapid through-put screening of ligands that specifically and selectively influence the activity of PR-A and/or PR-B. The ligands can be either agonists or antagonists of the progesterone receptor.

As used herein, the phrase "PR agonist ligand" or "PR agonist" refers to any compound that interacts with a PR and elicits an observable response. More particularly, a PR agonist can include, but is not limited to, steroidal or non-steroidal compounds; a protein, peptide, or nucleic acid that selectively binds to and activates or increases the activation of a progesterone receptor; and most commonly includes progesterone, progesterone analogs, and any suitable product of drug design (e.g., a mimetic of progesterone, or a synthetic progestin) which is characterized by its ability to agonize (e.g., stimulate, induce, increase, enhance) the biological activity of a naturally occurring progesterone receptor in a manner similar to the natural agonist, progesterone (e.g., by interaction/binding with and/or direct or indirect activation of a progesterone receptor). It is noted that the term "progestin" as used herein is generally intended to include progesterone as well as any progesterone analog, such as a synthetic progestin. Since the progesterone receptor is an intracellular receptor, a suitable agonist typically does not include an antibody or antigen binding fragment thereof, but to the extent that an antibody that selectively binds to and activates or increases the activation of a progesterone receptor can be designed and implemented as an agonist, such a compound is also contemplated. It is noted that the effect of the action of a given PR agonist on the expression of a downstream gene may be the *downregulation* of the gene or the suppression of the expression of a gene (e.g., when both isoforms of PR are present). Moreover, the action of the agonist on a PR may have undesirable consequences in one tissue type and beneficial consequences in another tissue type. However, the term agonist is intended to refer to the ability of the ligand to act on a progesterone receptor in a manner that is substantially similar to the action of the natural PR ligand, progesterone, on the progesterone receptor (described in more detail below). Typically, a PR agonist is identified under conditions wherein, in the absence of the agonist, the PR receptor is not activated, or is at least believed not to be in the presence of a compound that is known to activate the receptor, such as the natural ligand progesterone or a known progestin.

The phrase, "PR antagonist ligand" or "PR antagonist" refers to any compound which inhibits the effect of a PR agonist, as described above. More particularly, a PR antagonist is capable of associating with a progesterone receptor such that the biological activity of the receptor is decreased (e.g., reduced, inhibited, blocked, reversed, altered) in a manner that

is antagonistic (e.g., against, a reversal of, contrary to) to the action of the natural agonist, progesterone, on the receptor. Such a compound can include, but is not limited to, steroidal or non-steroidal compounds; a protein, peptide, or nucleic acid that selectively binds to and blocks access to the receptor by a natural or synthetic agonist ligand or reduces or inhibits the activity of a progesterone receptor; or a product of drug design that blocks the receptor or alters the biological activity of the receptor (e.g., an *antiprogestin,* which antagonizes the actions of progesterone). Again, since the progesterone receptor is an intracellular receptor, antibody antagonists are typically not practical, although if appropriate and feasible, their use is contemplated herein. It is noted that the action of a given PR antagonist on a given downstream gene via a PR may be to actually *upregulate* the gene. Moreover, the action of the antagonist on a PR may have undesirable consequences in one tissue type and beneficial consequences in another tissue type. However, the term antagonist is intended to refer to the ability of the ligand to act on a progesterone receptor in a manner that is antagonistic to the action of the natural PR ligand, progesterone, or a synthetic PR agonist, on the progesterone receptor. Typically, an antagonist is identified under control conditions wherein, in the absence of the antagonist, the progesterone receptor is stimulated, such as by the natural ligand, progesterone, or by any suitable progestin. In one embodiment, a PR antagonist can be identified by its ability to alter the regulation of downstream genes by the receptor in the *absence* of a known stimulator of the receptor. In this embodiment, ligand-independent regulators of progesterone receptor function can be identified by detecting effects on genes that are constitutively regulated by PR in the ligand-unactivated state.

According to the present invention, agonists and antagonist ligands can include any regulatory ligand or compound that has the above-mentioned characteristics with regard to regulation of a progesterone receptor. For example, agonists and antagonists can include steroidal and non-steroidal compounds, proteins and peptides, nucleic acid molecules, antibodies, and/or mimetics (e.g., products of drug design or combinatorial chemistry).

Natural sex steroid hormone agonists are low molecular weight ringed cyclopentanophenanthrene compounds that in mammals include progesterone, estrogens and androgens. Steroid agonists can be extracted from a variety of natural sources, including the ovaries and testes. With the aim of enhancing the properties of natural steroid compounds,

researchers have modified the cyclopentanophenanthrene structures and/or altered the substituent side-chains to generate semi-synthetic and synthetic steroidal and non-steroidal compounds. Non-steroidal compounds lack the classical cyclopentanophenanthrene structure. Nevertheless, all of these compounds – natural, semi-synthetic and synthetic, steroidal and non-steroidal compounds, bind to their respective nuclear receptors. Modified compounds can be either agonists or antagonists.

Progesterone is the natural "progestin" produced by the ovaries and adrenal glands of mammals. Semi-synthetic or synthetic analogs that have progesterone-like effects, can be either steroidal or non-steroidal. They are also included in the generic category called "progestins." Natural, semi-synthetic or synthetic progestins bind to intracellular, usually intranuclear, progesterone receptors. Such progestins can be either "agonists" or "antagonists" (antiprogestins). Both agonists and antagonists can have variable levels of activity of the receptors. An agonist can be strong or weak with many levels in between. An antagonist can also be strong or weak. Some antagonists may have "mixed" agonist/ antagonist properties. The present invention can screen for all of these types of progestins.

Other compounds in addition to steroidal and non-steroidal compounds can bind progesterone receptors. These include proteins and peptides, and nucleic acids and fragments thereof. Any compound that binds a receptor can be classified as a "ligand" of the receptor. If the ligand influences the activity of the progesterone receptor, the present invention can be used to screen for such ligand(s).

An isolated protein, according to the present invention, is a protein (including a peptide) that has been removed from its natural milieu (i.e., that has been subject to human manipulation) and can include purified proteins, partially purified proteins, recombinantly produced proteins, and synthetically produced proteins, for example. As such, "isolated" does not reflect the extent to which the protein has been purified. An isolated protein useful as an antagonist or agonist according to the present invention can be isolated from its natural source, produced recombinantly or produced synthetically. Smaller peptides useful as regulatory ligands are typically produced synthetically by methods well known to those of skill in the art. Regulatory ligands of the present invention can also include an antibody or antigen binding fragment that selectively binds to a progesterone receptor.

According to the present invention, the phrase "selectively binds to" refers to the ability of an antibody, antigen binding fragment or other binding partner (protein, peptide, nucleic acid) to preferentially bind to specified proteins. More specifically, the phrase "selectively binds" refers to the specific binding of one protein to another, wherein the level of binding, as measured by any standard assay, is statistically significantly higher than the background control for the assay.

Agonists and antagonists that are products of drug design can be produced using various methods known in the art. Various methods of drug design, useful to design mimetics or other regulatory compounds useful in the present invention are disclosed in Maulik et al., 1997, *Molecular Biotechnology: Therapeutic Applications and Strategies*, Wiley-Liss, Inc., which is incorporated herein by reference in its entirety. A PR agonist or antagonist can be obtained, for example, from molecular diversity strategies (a combination of related strategies allowing the rapid construction of large, chemically diverse molecule libraries), libraries of natural or synthetic compounds, in particular from chemical or combinatorial libraries (i.e., libraries of compounds that differ in sequence or size but that have the similar building blocks) or by rational, directed or random drug design. See for example, Maulik et al., *supra*.

In a molecular diversity strategy, large compound libraries are synthesized, for example, from peptides, oligonucleotides, natural or synthetic steroidal compounds, carbohydrates and/or natural or synthetic organic and non-steroidal molecules, using biological, enzymatic and/or chemical approaches. The critical parameters in developing a molecular diversity strategy include subunit diversity, molecular size, and library diversity. The general goal of screening such libraries is to utilize sequential application of combinatorial selection to obtain high-affinity ligands for a desired target, and then to optimize the lead molecules by either random or directed design strategies. Methods of molecular diversity are described in detail in Maulik, et al., ibid.

As used herein, the term "mimetic" is used to refer to any natural or synthetic steroidal compound, peptide, oligonucleotide, carbohydrate and/or natural or synthetic organic and non-steroidal molecule that is able to mimic the biological action of a naturally occurring or known synthetic progestin.

Methods and Products of the Present Invention:

One embodiment of the present invention relates to a method to identify agonist ligands of progesterone receptors. This method includes the steps of: (a) contacting a progesterone receptor with a putative agonist ligand, wherein the progesterone receptor is selected from the group consisting of progesterone receptor A (PR-A) and progesterone receptor B (PR-B), under conditions wherein, in the absence of the putative agonist ligand, the progesterone receptor is not activated; (b) detecting expression of at least one gene that is regulated by the progesterone receptor when the progesterone receptor is activated and, (c) comparing the expression of the at least one gene in the presence and in the absence of the putative agonist ligand, wherein detection of regulation of the expression of the at least one gene in the manner associated with activation of the progesterone receptor as set forth in (b) indicates that the putative agonist ligand is a progesterone receptor agonist. The gene can include any one or more of any of the following genes: (i) one or more of the genes that are selectively upregulated by PR-A chosen from a gene in Table 1; (ii) one or more of the genes that are selectively downregulated by PR-A chosen from a gene in Table 2; (iii) one or more of the genes that are selectively upregulated by PR-B chosen from a gene in Table 3; (iv) one or more of the genes that are selectively downregulated by PR-B chosen from a gene in Table 4; (v) one or more of the genes that are upregulated or downregulated in the same direction by both PR-A and PR-B chosen from a gene in Table 5; (vi) one or more of the genes that are reciprocally regulated by PR-A and PR-B chosen from a gene in Table 6; and, (vii) one or more of the genes that are regulated by one of either PR-A or PR-B, wherein the regulation of the gene is altered when the other of the PR-A or PR-B is present, such a gene being chosen from a gene in Table 7.

Another embodiment of the present invention relates to a method to identify antagonists of progesterone receptor. This method includes the steps of: (a) contacting a progesterone receptor with a putative antagonist ligand, wherein the progesterone receptor is selected from the group consisting of progesterone receptor A (PR-A) and progesterone receptor B (PR-B), under conditions wherein, in the absence of said putative antagonist ligand, said progesterone receptor is activated (i.e., before, simultaneously with or after the contact of the receptor with the putative regulatory ligand); (b) detecting expression of at

least one gene that is regulated by the progesterone receptor when the progesterone receptor is activated; and, (c) comparing the expression of the at least one gene in the presence and in the absence of the putative antagonist ligand. Detection of inhibition or reversal of the regulation of expression of the at least one gene as compared to the regulation of expression of the at least one gene in the manner associated with activation of the progesterone receptor as set forth in (b), indicates that the putative antagonist ligand is a progesterone receptor antagonist. The gene(s) to be detected in step (b) are chosen from one or more of the following genes: (i) one or more of the genes that are selectively upregulated by PR-A chosen from a gene in Table 1; (ii) one or more of the genes that are selectively downregulated by PR-A chosen from a gene in Table 2; (iii) one or more of the genes that are selectively upregulated by PR-B chosen from a gene in Table 3; (iv) one or more of the genes that are selectively downregulated by PR-B chosen from a gene in Table 4; (v) one or more of the genes that are upregulated or downregulated by both PR-A and PR-B chosen from a gene in Table 5; (vi) one or more of the genes that are reciprocally regulated by PR-A and PR-B chosen from a gene in Table 6; and, (vii) one or more of the genes that are regulated by one of the PR-A or the PR-B, wherein regulation of the gene is altered when the other of the PR-A or PR-B is expressed by the same cell, chosen from a gene in Table 7. In one embodiment, the progesterone receptor is activated by contacting the receptor with a compound that activates the receptor, the step of contacting being performed prior to, simultaneously with, or after the step of contacting of (a).

The steps of the method of the present invention will now be described in some detail for these embodiments of the invention; however, this discussion generally applies to other methods of identifying various ligands of progesterone receptors as described below.

As used herein, the term "putative regulatory compound" or "putative regulatory ligand" refers to compounds having an unknown regulatory activity, at least with respect to the ability of such compounds to regulate progesterone receptors as described herein.

In the method of identifying a regulatory ligand (i.e., an agonist or an antagonist) according to the present invention, the method can be a cell-based assay, or non-cell-based assay. In one embodiment, the progesterone receptor is expressed by a cell (i.e., a cell-based assay). In another embodiment the progesterone receptor is in a cell lysate, is in isolated cell

nuclei, or is purified or produced free of cells. The progesterone receptor can be a PR-A, a PR-B, or a combination of PR-A and PR-B. One advantage of the present invention is that, given the knowledge of the isoform regulation of the various downstream genes disclosed herein, one can screen for ligands of the progesterone receptor, including screening for isoform specific ligands, using cells that express both receptors. Prior to the present invention, it was impossible to distinguish between the effects of one isoform or the other, because most cells express both isoforms.

In one embodiment, the conditions under which a receptor according to the present invention is contacted with a putative regulatory ligand, such as by mixing, are conditions in which the receptor is not stimulated (activated) if essentially no regulatory ligand is present. For example, such conditions include normal culture conditions in the absence of a known stimulatory compound (a stimulatory compound being, for example, the natural ligand for the receptor (progesterone), a stimulatory peptide, or other equivalent stimulus, such as a synthetic progestin). The putative regulatory ligand is then contacted with the receptor. In this embodiment, the step of detecting is designed to indicate whether the putative regulatory ligand alters the biological activity of the receptor as compared to in the absence of the putative regulatory ligand (i.e., the background level), as determined by the effects of the contact between the ligand and the receptor on the expression of downstream genes as described herein.

In an alternate embodiment, the conditions under which a progesterone receptor according to the present invention is contacted with a putative regulatory ligand, such as by mixing, are conditions in which the receptor is normally stimulated (activated) if essentially no regulatory ligand is present. Such conditions can include, for example, contact of said receptor with a stimulator molecule (a stimulatory compound being, e.g., the natural ligand for the receptor (progesterone), a stimulatory peptide, or other equivalent stimulus, such as a synthetic progestin) which binds to the receptor and causes the receptor to become activated. In this embodiment, the putative regulatory ligand can be contacted with the receptor prior to, or simultaneously with, the contact of the receptor with the stimulatory compound (e.g., to determine whether the putative regulatory ligand blocks or otherwise inhibits the stimulation of the progesterone receptor by the stimulatory compound), or after

contact of the receptor with the stimulatory compound (e.g., to determine whether the putative regulatory ligand downregulates, or reduces the activation of the receptor).

The present methods involve contacting the progesterone receptor with the ligand being tested for a sufficient time to allow for interaction, activation or inhibition of the receptor by the ligand. The period of contact with the ligand being tested can be varied depending on the result being measured, and can be determined by one of skill in the art. For example, for binding assays, a shorter time of contact with the compound being tested is typically suitable, than when activation is assessed, and particularly, when the expression of downstream genes is assessed. The methods of the present invention detect the expression of downstream genes and therefore, the time of incubation is dependent upon the time required to achieve expression of the downstream genes. Such a time period is typically at least 2 hours, and more preferably at least 4 hours, and more preferably at least 6 hours, although the time can be extended, if necessary to detect expression of a selected downstream gene. As used herein, the term "contact period" refers to the time period during which the progesterone receptor is in contact with the ligand being tested. The term "incubation period" refers to the entire time during which the cells expressing the receptor, for example, are allowed to grow prior to evaluation, or the time during which genes affected by activation of the progesterone receptor are allowed to be expressed, and such time period can be inclusive of the contact period. Thus, the incubation period includes all of the contact period and may include a further time period during which the compound being tested is not present, or is no longer being supplied to the receptor, but during which gene expression is continuing (in the case of a cell based assay) prior to scoring. The incubation time for growth of cells can vary but is sufficient to allow for the binding of the progesterone receptor, the activation or inhibition of the receptor, and the effect on the expression of the downstream genes regulated by the receptor. It will be recognized that shorter incubation times are preferable because compounds can be more rapidly screened.

In accordance with the present invention, a cell-based assay is conducted under conditions which are effective to screen for regulatory compounds useful in the method of the present invention. Effective conditions include, but are not limited to, appropriate media, temperature, pH and oxygen conditions that permit the growth of the cell that expresses the

receptor. An appropriate, or effective, medium refers to any medium in which a cell that naturally or recombinantly expresses a progesterone receptor, when cultured, is capable of cell growth and expression of the progesterone receptor. Such a medium is typically a solid or liquid medium comprising growth factors and assimilable carbon, nitrogen and phosphate sources, as well as appropriate salts, minerals, metals and other nutrients, such as vitamins. Culturing is carried out at a temperature, pH and oxygen content appropriate for the cell. Such culturing conditions are within the expertise of one of ordinary skill in the art. Exemplary cells expressing progesterone receptors are described in the Examples, and in detail in (Sartorius *et al.*, *Cancer Res.* 54, 3668-3877 (1994)).

Cells that are useful in the cell-based assays of the present invention include any cell that expresses a progesterone receptor of the isoform A, isoform B, or a combination of PR-A and PR-B. Such cells include cells that naturally express progesterone receptors, or cells that express progesterone receptors by recombinant technology. Such cells preferably include, but are not limited to mammalian cells, which can originate from the breast or any other tissue. For example, tissues containing cells that are known to express the progesterone receptor naturally include, but are not limited to, breast, uterus, bone, cartilage, cardiovascular tissues, heart, lung, brain, meninges, pituitary, ovary, oocyte, corpus luteum, oviduct, fallopian tubes, T lymphocytes, B lymphocytes, thymocytes, salivary gland, placenta, skin, gut, pancreas, liver, testis, epididymis, bladder, urinary tract, eye, and teeth. Cells suitable for use in a cell-based assay include normal or malignant cells, as well as cells that are not malignant, but which are abnormal, such as cells from a non-malignant tissue that is otherwise diseased (e.g., tissues from endometriosis and leiomyoma of the uterus, fibrocystic disease of the breast, polycystic ovary). Other suitable cells are cells that express PR-A, PR-B, or both isoforms, as a result of recombinant technology. Such cells were used to discover the PR downstream genes of the present invention and are described in detail in Sartorius et al. (Sartorius *et al.*, *Cancer Res.* 54, 3668-3877 (1994)). Other suitable cells are cells that express a PR-A and/or a PR-B transgene (i.e., cells isolated from a transgenic animal), or cells that have a germline deletion of one of the PR isoforms, but not the other (i.e., cells from a PR-A or PR-B knockout animal).

According to the present invention, the method includes the step of detecting the expression of at least one, and preferably more than one, of the downstream genes that have now been shown to be regulated by progesterone receptors by the present inventors. As used herein, the term "expression", when used in connection with detecting the expression of a downstream gene of the present invention, can refer to detecting transcription of the gene and/or to detecting translation of the gene. To detect expression of a downstream gene refers to the act of actively determining whether a gene is expressed or not. This can include determining whether the gene expression is upregulated as compared to a control, downregulated as compared to a control, or unchanged as compared to a control. Therefore, the step of detecting expression does not require that expression of the gene actually is upregulated or downregulated, but rather, can also include detecting that the expression of the gene has not changed (i.e., detecting no expression of the gene or no change in expression of the gene).

The present method includes the step of detecting the expression of at least one gene that is regulated by a progesterone receptor when the receptor is activated, as set forth in detail above. In a preferred embodiment, the step of detecting includes detecting the expression of at least 2 genes, and preferably at least 3 genes, and more preferably at least 4 genes, and more preferably at least 5 genes, and more preferably at least 6 genes, and more preferably at least 7 genes, and more preferably at least 8 genes, and more preferably at least 9 genes, and more preferably at least 10 genes, and more preferably at least 11 genes, and more preferably at least 12 genes, and more preferably at least 13 genes, and more preferably at least 14 genes, and more preferably at least 15 genes, and so on, in increments of one, up to detecting expression of all of the downstream genes disclosed herein. Analysis of a number of genes greater than 1 can be accomplished simultaneously, sequentially, or cumulatively.

In the method of identifying an agonist or an antagonist of a progesterone receptor of the present invention, the gene(s) to be detected are preferably selected from the genes described in any one or more of Tables 1-7. These tables disclose genes that are regulated by progesterone receptors, and particularly, these tables disclose the manner in which the genes are regulated by the PR isoforms when the progesterone receptor is activated (i.e., by

a stimulator of the receptor). The genes to be detected can include one or more of: (1) genes that are selectively (i.e., exclusively or uniquely) upregulated by PR-A (Table 1); (2) genes that are selectively downregulated by PR-A (Table 2); (3) genes that are selectively upregulated by PR-B (Table 3); (4) genes that are selectively downregulated by PR-B (Table 4); (5) genes that are upregulated or downregulated in the same direction by both PR-A and PR-B (Table 5); (6) genes that are reciprocally regulated by PR-A and PR-B (Table 6); and (7) genes that are regulated by one of the PR isoforms, wherein such regulation is altered when the other PR isoform is present (e.g., the expression of the gene is either up- or downregulated in the presence of both receptors relative to the expression level of the gene in the presence of only one receptor) (Table 7). In one embodiment, the method further includes the additional detection of the expression of one or more genes that were previously known to be regulated by progesterone, but for which the PR isoform regulation was not known until the present invention. Such genes are disclosed in Table 8.

It is to be understood that the organization of various genes into the present tables is for purposes of clarity and identification of various genes on the basis of the manner in which the gene is regulated by a progesterone receptor isoform. The selection of genes to be detected in any given method can include any one or more of the genes in any one or more of the Tables, and can include the detection of any combination of two or more of the genes in any one or more of the Tables. It is not mandatory that a given assay be restricted to the detection of all of the various genes in a single table, or to one gene in each table. In addition, with regard to Tables 1-7, it is believed that these tables encompass genes that have been identified by the present inventors to be regulated by progesterone receptors, but which have not previously been described as being regulated by progesterone. However, in the event that one or more of the genes in Tables 1-7 is found to have previously been known to be regulated by progesterone, the removal of such gene from these tables and the placement of such gene into Table 8, is explicitly contemplated. This rationale also applies to the genes of Table 16, which are believed to include all of those genes identified by the inventors that were previously known to be involved in breast cancer or mammary development. It is expressly contemplated that other genes from Tables 1-7 or 9-15 can be added to Table 16, if required for accuracy. Tables 9-15 include all of the genes identified

by the present inventors as being regulated by progesterone receptors (organized by isoform regulation, as for Tables 1-7), and, as discussed previously herein, include genes that were previously known to be regulated by progesterone.

Given the knowledge of the genes regulated by progesterone receptors according to the present invention, one of skill in the art will be able to select one or more genes to detect in a method of the present invention, and the selection of the one or more genes can be determined by different factors. For example, certain subsets of the genes are useful for detecting genes regulated by PR-A exclusively (i.e., genes in Tables 1, 2, 9 and 10). Other subsets of genes are useful for detecting genes regulated by PR-B exclusively (i.e., genes in Tables 3, 4, 11 and 12). One of skill in the art may wish to detect genes disclosed herein that are related to a particular function, to a particular tissue-type, or that are associated (or likely to be associated) with a particular disease or condition. One of skill in the art may also wish to select genes on the basis of the change in expression level in the presence of progesterone (i.e., and therefore activation of the PR) as compared to in the absence of progesterone.

In one aspect of the methods of the present invention, the method of the present invention includes detecting genes of the present invention that are related by function. For example, Table 17 provides a listing of the various genes identified by the present inventors, categorized by function. Therefore, one could screen functional sets of genes to make a specific determination about a given cell or tissue that expresses a progesterone receptor, or to identify a ligand that has an action that might be correlated with a functional gene. For example, one could use subsets of the disclosed genes to screen a tumor for the likelihood that it will metastasize by screening the genes in the "cell adhesion or cytoskeletal interaction" group of Table 17. Other uses for screening functional groups will be apparent to those of skill in the art.

In another aspect, one could detect genes that are of interest in a particular tissue type. Examples of such genes are disclosed below in the discussion regarding the identification of tissue-specific ligands of progesterone receptors.

In another aspect, one could detect those genes that are associated with a particular disease, such as breast cancer. An exemplary grouping of genes that are regulated by progesterone receptors (as disclosed herein) and that were previously known to be involved

in breast cancer or mammary gland development, are shown in Table 16. In one embodiment, one may be interested in detecting those genes listed in Table 16 which are not also listed in Table 8.

In another aspect, it may be desirable to select those genes for detection that are particularly highly regulated by progesterone receptors in that they display the largest increases or decreases in expression levels in the presence of progesterone as compared to in the absence of progesterone. The detection of such genes can be advantageous because the endpoint may be more clear and require less quantitation. The relative expression levels of the genes identified in the present invention are listed in the tables. In these tables, the fold increase or decrease in expression of the gene upon treatment of the progesterone receptor with progesterone for 6 hours is indicated. The fold increase or decrease was made with respect to the background level of expression of the gene, which in some cases, was undetectable (i.e., the gene was not detected at all in the absence of progesterone, but was detected in the presence of progesterone). Therefore, in one embodiment, one of skill in the art might choose to detect genes that exhibited a fold increase above background of at least 2. In another embodiment, one of skill in the art might choose to detect genes that exhibited a fold increase or decrease above background of at least 3, and in another embodiment at least 4, and in another embodiment at least 5, and in another embodiment at least 6, and in another embodiment at least 7, and in another embodiment at least 8, and in another embodiment at least 9, and in another embodiment at least 10 or higher fold changes. It is noted that fold increases or decreases are not typically compared from one gene to another, but with reference to the background level for that particular gene.

In order to determine whether a putative regulatory compound is an agonist or antagonist of PR as defined herein, it is necessary to know how a given gene is regulated by the PR so that one can compare the results in the presence and absence of the putative regulatory ligand to the gene expression profile produced by an activated receptor. This allows the investigator to thereby detect whether the contact of the receptor with the putative ligand results in a profile of gene expression that is substantially similar to the profile of gene expression of an activated PR (i.e., agonist action), or whether contact of the receptor with

the putative ligand results in a profile of gene expression that is an inhibition, or reversal, of the profile of gene expression of an activated PR (i.e., antagonist action).

In one aspect of the method of the present invention, the step of detecting can include the detection of one or more reporter genes that are linked to promoters of one or more downstream genes according to the present invention. In this embodiment, the transcriptional read-out can use one, two or more promoters of any of the genes of this invention, linked to any of several reporter constructs, which are introduced into cells by any of several established transfection or infection methods, including, but not limited to, calcium phosphate transfection, transformation, electroporation, microinjection, lipofection, adsorption, infection (e.g., by a viral vector) and protoplast fusion. The cells can be naturally PR-positive (containing both PRs), or they can stably or transiently express either one or both of the two PR-isoforms. The cells can be exposed to the test ligands (i.e., the putative regulatory ligands) for different times and/or concentrations, and transcription of the PR-responsive promoter(s) of the downstream genes disclosed in this invention can be quantified.

In another aspect of this method of the present invention, cells expressing a PR as described above are exposed to the unknown test ligands at various concentrations and for various periods of time. The transcriptional read-out can be expression of one, two or more of the genes of this invention, which are endogenously regulated in the cells. Expression of their transcripts and/or proteins is measured by any of a variety of known methods in the art several of which are exemplified in the Examples section. For RNA expression, methods include but are not limited to: extraction of cellular mRNA and northern blotting using labeled probes that hybridize to transcripts encoding all or part of one or more of the genes of this invention; amplification of mRNA expressed from one or more of the genes of this invention using gene-specific primers and reverse transcriptase - polymerase chain reaction, followed by quantitative detection of the product by any of a variety of means; extraction of total RNA from the cells, which is then labeled and used to probe cDNAs or oligonucleotides encoding all or part of the PR-responsive genes of this invention, arrayed on any of a variety of surfaces.

Methods to measure protein expression levels of selected genes of this invention, include, but are not limited to: western blotting, immunocytochemistry, flow cytometry or other immunologic-based assays; assays based on a property of the protein including but not limited to DNA binding, ligand binding, or interaction with other protein partners.

Nucleic acid arrays are particularly useful for detecting the expression of the downstream genes of the present invention. The production and application of high-density arrays in gene expression monitoring have been disclosed previously in, for example, WO 97/10365; WO 92/10588; U.S. Patent No. 6,040,138; U.S. 5,445,934; or WO95/35505, all of which are incorporated herein by reference in their entireties. Also for examples of arrays, see Hacia *et al.* (1996) *Nature Genetics* 14:441-447; Lockhart *et al.* (1996) Nature Biotechnol. 14:1675-1680; and De Risi *et al.* (1996) *Nature Genetics* 14:457-460. In general, in an array, an oligonucleotide, a cDNA, or genomic DNA, that is a portion of a known gene occupies a known location on a substrate. A nucleic acid target sample is hybridized with an array of such oligonucleotides and then the amount of target nucleic acids hybridized to each probe in the array is quantified. One preferred quantifying method is to use confocal microscope and fluorescent labels. The *Affymetrix GeneChip™ Array* system (Affymetrix, Santa Clara, Calif.) and the *Atlas™ Human cDNA Expression Array* system are particularly suitable for quantifying the hybridization; however, it will be apparent to those of skill in the art that any similar systems or other effectively equivalent detection methods can also be used. The Examples section describes the use of these two different array systems. In a particularly preferred embodiment, one can use the knowledge of the genes described herein to design novel arrays of polynucleotides, cDNAs or genomic DNAs for screening methods described herein. Such novel pluralities of polynucleotides are contemplated to be a part of the present invention and are described in detail below.

Suitable nucleic acid samples for screening on an array contain transcripts of interest or nucleic acids derived from the transcripts of interest (i.e., transcripts derived from the PR-regulated genes of the present invention). As used herein, a nucleic acid derived from a transcript refers to a nucleic acid for whose synthesis the mRNA transcript or a subsequence thereof has ultimately served as a template. Thus, a cDNA reverse transcribed from a transcript, an RNA transcribed from that cDNA, a DNA amplified from the cDNA, an RNA

transcribed from the amplified DNA, etc., are all derived from the transcript and detection of such derived products is indicative of the presence and/or abundance of the original transcript in a sample. Thus, suitable samples include, but are not limited to, transcripts of the gene or genes, cDNA reverse transcribed from the transcript, cRNA transcribed from the cDNA, DNA amplified from the genes, RNA transcribed from amplified DNA, and the like.

Preferably, the nucleic acids for screening are obtained from a homogenate of cells or tissues or other biological samples. Preferably, such sample is a total RNA preparation of a biological sample. More preferably in some embodiments, such a nucleic acid sample is the total mRNA isolated from a biological sample. Biological samples may be of any biological tissue or fluid or cells from any organism. Frequently the sample will be a "clinical sample" which is a sample derived from a patient, such as a breast tumor sample from a patient. Typical clinical samples include, but are not limited to, sputum, blood, blood cells (e.g., white cells), tissue or fine needle biopsy samples, urine, peritoneal fluid, and pleural fluid, or cells therefrom. Biological samples may also include sections of tissues, such as frozen sections or formalin fixed sections taken for histological purposes.

In one embodiment, it is desirable to amplify the nucleic acid sample prior to hybridization. One of skill in the art will appreciate that whatever amplification method is used, if a quantitative result is desired, care must be taken to use a method that maintains or controls for the relative frequencies of the amplified nucleic acids to achieve quantitative amplification. Methods of "quantitative" amplification are well known to those of skill in the art. For example, quantitative PCR involves simultaneously co-amplifying a known quantity of a control sequence using the same primers. This provides an internal standard that may be used to calibrate the PCR reaction. The high-density array may then include probes specific to the internal standard for quantification of the amplified nucleic acid. Other suitable amplification methods include, but are not limited to polymerase chain reaction (PCR) Innis, et al., PCR Protocols. A guide to Methods and Application. Academic Press, Inc. San Diego, (1990)), ligase chain reaction (LCR) (see Wu and Wallace, Genomics, 4: 560 (1989), Landegren, et al., Science, 241: 1077 (1988) and Barringer, et al., Gene, 89: 117 (1990), transcription amplification (Kwoh, et al., Proc. Natl. Acad. Sci. USA, 86: 1173

(1989)), and self-sustained sequence replication (Guatelli, et al, Proc. Nat. Acad. Sci. USA, 87: 1874 (1990)).

Nucleic acid hybridization simply involves contacting a probe and target nucleic acid under conditions where the probe and its complementary target can form stable hybrid duplexes through complementary base pairing. As used herein, hybridization conditions refer to standard hybridization conditions under which nucleic acid molecules are used to identify similar nucleic acid molecules. Such standard conditions are disclosed, for example, in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Labs Press, 1989. Sambrook et al., *ibid.*, is incorporated by reference herein in its entirety (see specifically, pages 9.31-9.62). In addition, formulae to calculate the appropriate hybridization and wash conditions to achieve hybridization permitting varying degrees of mismatch of nucleotides are disclosed, for example, in Meinkoth et al., 1984, *Anal. Biochem.* 138, 267-284; Meinkoth et al., *ibid.*, is incorporated by reference herein in its entirety. Nucleic acids that do not form hybrid duplexes are washed away from the hybridized nucleic acids and the hybridized nucleic acids can then be detected, typically through detection of an attached detectable label. It is generally recognized that nucleic acids are denatured by increasing the temperature or decreasing the salt concentration of the buffer containing the nucleic acids. Under low stringency conditions (e.g., low temperature and/or high salt) hybrid duplexes (e.g., DNA:DNA, RNA:RNA, or RNA:DNA) will form even where the annealed sequences are not perfectly complementary. Thus specificity of hybridization is reduced at lower stringency. Conversely, at higher stringency (e.g., higher temperature or lower salt) successful hybridization requires fewer mismatches.

High stringency hybridization and washing conditions, as referred to herein, refer to conditions which permit isolation of nucleic acid molecules having at least about 90% nucleic acid sequence identity with the nucleic acid molecule being used to probe in the hybridization reaction (i.e., conditions permitting about 10% or less mismatch of nucleotides). One of skill in the art can use the formulae in Meinkoth et al., 1984, *Anal. Biochem.* 138, 267-284 (incorporated herein by reference in its entirety) to calculate the appropriate hybridization and wash conditions to achieve these particular levels of nucleotide mismatch. Such conditions will vary, depending on whether DNA:RNA or DNA:DNA

hybrids are being formed. Calculated melting temperatures for DNA:DNA hybrids are 10°C less than for DNA:RNA hybrids. In particular embodiments, stringent hybridization conditions for DNA:DNA hybrids include hybridization at an ionic strength of 6X SSC (0.9 M Na^+) at a temperature of between about 20°C and about 35°C, more preferably, between about 28°C and about 40°C, and even more preferably, between about 35°C and about 45°C. In particular embodiments, stringent hybridization conditions for DNA:RNA hybrids include hybridization at an ionic strength of 6X SSC (0.9 M Na^+) at a temperature of between about 30°C and about 45°C, more preferably, between about 38°C and about 50°C, and even more preferably, between about 45°C and about 55°C. These values are based on calculations of a melting temperature for molecules larger than about 100 nucleotides, 0% formamide and a G + C content of about 40%. Alternatively, T_m can be calculated empirically as set forth in Sambrook et al., *supra*, pages 9.31 to 9.62.

The hybridized nucleic acids are detected by detecting one or more labels attached to the sample nucleic acids. The labels may be incorporated by any of a number of means well known to those of skill in the art. Detectable labels suitable for use in the present invention include any composition detectable by spectroscopic, photochemical, biochemical, immunochemical, electrical, optical or chemical means. Useful labels in the present invention include biotin for staining with labeled streptavidin conjugate, magnetic beads (e.g., Dynabeads.TM.), fluorescent dyes (e.g., fluorescein, texas red, rhodamine, green fluorescent protein, and the like), radiolabels (e.g., ^3H, ^{125}I, ^{35}S, ^{14}C, or ^{32}P), enzymes (e.g., horse radish peroxidase, alkaline phosphatase and others commonly used in an ELISA), and colorimetric labels such as colloidal gold or colored glass or plastic (e.g., polystyrene, polypropylene, latex, etc.) beads. Means of detecting such labels are well known to those of skill in the art. Thus, for example, radiolabels may be detected using photographic film or scintillation counters, fluorescent markers may be detected using a photodetector to detect emitted light. Enzymatic labels are typically detected by providing the enzyme with a substrate and detecting the reaction product produced by the action of the enzyme on the substrate, and colorimetric labels are detected by simply visualizing the colored label.

The term "quantifying" or "quantitating" when used in the context of quantifying transcription levels of a gene can refer to absolute or to relative quantification. Absolute

quantification may be accomplished by inclusion of known concentration(s) of one or more target nucleic acids and referencing the hybridization intensity of unknowns with the known target nucleic acids (e.g. through generation of a standard curve). Alternatively, relative quantification can be accomplished by comparison of hybridization signals between two or more genes, or between two or more treatments to quantify the changes in hybridization intensity and, by implication, transcription level.

In one aspect of the present method, *in vitro* cell based assays may be designed to screen for compounds that affect the regulation of genes by a progesterone receptor at either the transcriptional or translational level. One, two or more promoters of the genes of this invention can be used to screen unknown ligands for their ability to selectively regulate transcription *in vitro* via PR-A or PR-B. Promoters of the selected genes can be linked to any of several reporters (including but not limited to chloramphenicol acetyl transferase, or luciferase) that measure transcriptional read-out. The promoters can be tested as pure DNA, or as DNA bound to chromatin proteins. Ligands at different concentrations and under different assay conditions can be screened for their ability to either up- or downregulate transcription of the selected genes, under the control of either PR-A, PR-B or both. In this embodiment, cells expressing progesterone receptors or cell lysates comprising progesterone receptors are contacted with a putative regulatory ligand for a time sufficient to act on the receptor. The cells or cell lysates contain one, two or more promoters of the selected genes that are linked to any of several reporters, and the transcription or translation of the reporter genes is measured. Appropriate cells are preferably prepared from any cell type that naturally expresses the progesterone receptor or that recombinantly expresses the progesterone receptor, thereby ensuring that the cells contain the transcription factors required for transcription. The screen can be used to identify ligands that modulate the expression of the reporter construct. In such screens, the level of reporter gene expression is determined in the presence of the test ligand and compared to the level of expression in the absence of the test ligand, or the test ligand is compared to a known ligand, such as progesterone.

In one aspect of the present method, the step of detecting can include detecting the expression of one or more downstream genes of the invention in intact animals or tissues

obtained from such animals. Mammalian (i.e. mouse, rat, monkey) or non-mammalian (ie. chicken) species that express PRs in their tissues and elaborate progesterone, can be the test animals. The unknown test ligand is introduced into intact or castrated animals by any of a variety of oral, intravenous, intramuscular, subdermal or other routes, for a variety of treatment times or concentrations. The tissues to be surveyed can be either normal or malignant progesterone targets (including but not limited to the mammary glands, mammary cancers, uterus, or endometrial cancers). The presence and quantity of endogenous mRNA or protein expression of one, two or more of the genes of this invention can be measured in those progesterone target tissues. The gene markers can be measured in tissues that are fresh, frozen, fixed or otherwise preserved. They can be measured in cytoplasmic or nuclear organ-, tissue- or cell-extracts; or in cell membranes including but not limited to plasma, cytoplasmic, mitochondrial, golgi or nuclear membranes; in the nuclear matrix; or in cellular organelles and their extracts including but not limited to ribosomes, nuclei, nucleoli, mitochondria, or golgi. Assays for endogenous expression of mRNAs or proteins encoded by the genes of this invention can be performed as described above. Alternatively, intact transgenic animals can be generated for ligand screening. Animals can be genetically manipulated to express the promoters of one, two or more of the genes of this invention linked to one or more reporters such as X-gal. After treatment of the animals with the test unknown ligands, expression of galactosidase can be measured colorimetrically in normal or malignant progesterone target organs, or tissues containing PRs, or in organs or tissues during development. Ligands that activate through either PR-A or PR-B can be identified by their ability to regulate the appropriate selective gene promoter.

The method of the present invention includes a step of comparing the results of detecting the expression of the one or more downstream genes in the presence and in the absence of the putative regulatory ligand, in order to determine whether any observed change in expression is due to the presence of the putative regulatory compound. The step of comparing further includes comparing the expression of the one or more downstream genes detected in the presence of the ligand to the manner of expression of the genes that is associated with the activation of the progesterone receptor when the receptor is activated (described in detail below). As discussed above, the present inventors have identified the

expression profile of multiple genes that are regulated by PR, including the manner in which the genes are regulated (i.e., by which PR isoform, and in which direction by such isoform). Therefore, one can determine whether the contact of the receptor with the putative ligand results in a profile of gene expression that is substantially similar to the profile of gene expression of an activated PR (i.e., agonist action), or whether contact of the receptor with the putative ligand results in a profile of gene expression that is an inhibition, or reversal, of the profile of gene expression of an activated PR (i.e., antagonist action). According to the present invention, a putative test ligand is determined to be a regulator of PR if the expression of the gene or genes detected after contact of the PR with the ligand is statistically significantly altered (i.e., up or down) from the expression detected in the profile of a PR that has been activated by progesterone, or an equivalent agonist. The expression profiles for the genes in Tables 1-19 were determined by evaluating PR that had been activated by progesterone after 6 hours.

A PR agonist is identified by detecting an expression profile in the presence of the agonist that, at a minimum, regulates the expression of the gene in the same direction (i.e, upregulation or downregulation) as it is regulated by an activated progesterone receptor (e.g., the manner of expression of the gene as indicated in Tables 1-7, 9-15 or 18 and 19). More specifically, and by way of example, detection of the regulation of the expression of the gene in the "manner" associated with the activation of the PR (i.e., the natural activation of the PR), at a minimum, refers to the detection of the upregulation of a gene that has now been shown by the present inventors to be selectively upregula3ted by PR-A (genes in Tables 1 and 9) when the receptor is in the presence of the putative agonist, as compared to in the absence of the putative agonist. Similarly, an agonist is identified when the expression of a gene from Tables 2 or 10 is detected to be downregulated in the presence of the putative agonist as compared to in the absence of the agonist. Such downregulation also indicates that, at a minimum, the agonist regulated the PR-A isoform. In a preferred embodiment, the agonist regulates the expression of the gene in the same direction and to at least about 10%, and more preferably at least 20%, and more preferably at least 25%, and more preferably at least 30%, and more preferably at least 35%, and more preferably at least 40%, and more preferably at least 45%, and more preferably at least 50%, and preferably at least 55%, and

more preferably at least 60%, and more preferably at least 65%, and more preferably at least 70%, and more preferably at least 75%, and more preferably at least 80%, and more preferably at least 85%, and more preferably at least 90%, and more preferably at least 95%, of the level of expression that is induced by a progesterone receptor that has been activated by progesterone. In a particularly preferred embodiment, an agonist regulates the expression of the gene in the same direction and to a level of expression that is substantially equal to or greater than the level of expression that is induced by a progesterone receptor that has been activated by progesterone. The level of expression is determined with reference to the expression of the gene in the absence of the putative regulatory compound, or in the absence of progesterone, in the case of the control. The level of expression is then compared to the level of expression of the control, or the level of expression that is expected from the control.

A PR antagonist is identified by detecting an expression profile in the presence of the antagonist that, at a minimum, regulates the expression of the gene in the opposite direction (i.e, upregulation instead of downregulation) than the gene is regulated by an activated progesterone receptor (e.g., the manner of expression of the gene as indicated in Tables 1-7, 9-15 or 18 and 19), or causes a statistically significant reduction in the expression level of the gene as compared to the expression level of the gene when it is activated by progesterone, or prevents the regulation of the gene as compared to the regulation of the gene when the receptor is activated by progesterone. In the antagonist screening embodiments, the putative antagonists are screened against a PR that is activated, and so in the absence of the putative antagonist, the expression profile of the genes should be substantially the same as the expression profile set forth in Tables 1-7, 9-15 and 18-19). Therefore, any statistically significant decrease (inhibition) in the expression level of the gene or a reversal of the direction of expression of the gene in the presence of the putative antagonist as compared to in the absence of the antagonist, indicates that the putative ligand is an antagonist. In a preferred embodiment, the antagonist inhibits the expression of the detected gene by at least 5%, and more preferably at least 10%, and more preferably at least 15%, and more preferably at least 20%, and more preferably at least 25%, and more preferably at least 30%, and more preferably at least 40%, and more preferably at least 50%, and more preferably at least 60%, and more preferably at least 70%, and more preferably at least 80%, and more preferably at

least 90%, as compared to the level of expression that is induced by the activated progesterone receptor in the absence of the putative antagonist. In one embodiment, an antagonist regulates the expression of the gene in the opposite direction (i.e., reverses the expression) as compared to the expression of the gene induced by the activated progesterone receptor in the absence of the putative antagonist.

It will be appreciated by those of skill in the art that differences between the expression of genes regulated by the putative ligand (via the PR) and the expression of genes regulated by the natural ligand (via the PR) may be small or large. Some small differences may be very reproducible and therefore the ligand identified by the method can be useful. For other purposes, large differences may be desirable for ease of detection of the regulatory activity. It will be therefore appreciated that the exact boundary between what is called an agonist and what is called an antagonist can shift, depending on the goal of the screening assay. For some assays it may be useful to set threshold levels of change. For other purposes the putative antagonist ligand may simply have a lower level of activity than an agonist ligand (e.g. a test ligand having 10% of the activity of an agonist can be an antagonist of that agonist). This may depend on the technique being used for detection as well as on the number of genes which are being tested. One of skill in the art can readily determine the criteria for selection of suitable antagonists.

Given the knowledge of the gene expression profiles of the present invention as set forth in Tables 1-7, 9-15 and 18-19, one of skill in the art can, for the first time, identify isoform-specific regulators of progesterone receptors. Therefore, one embodiment of the present invention relates to a method to identify isoform-specific agonists of progesterone receptors. This method includes the steps of: (a) contacting a progesterone receptor with a putative agonist ligand, wherein the progesterone receptor is selected from the group consisting of progesterone receptor A (PR-A) and progesterone receptor B (PR-B), under conditions wherein in the absence of the putative agonist ligand, the progesterone receptor is not activated; (b) detecting expression of at least one gene that is selectively regulated by the progesterone receptor when the progesterone receptor is activated, and (c) comparing the expression of the at least one gene in the presence and in the absence of the putative agonist ligand. In this embodiment, the at least one gene is selected from the group consisting of:

(i) at least one gene that is exclusively upregulated or downregulated by PR-A, chosen from a Table selected from the group consisting of Table 1 and Table 2; and, (ii) at least one gene that is exclusively upregulated or downregulated by PR-B chosen from a Table selected from the group consisting of Table 3 and Table 4. Detection of regulation of the expression of the at least one gene in the manner associated with activation of the progesterone receptor as set forth in (i) but not (ii), indicates that the putative agonist ligand is a PR-A-specific agonist, and wherein detection of regulation of the expression of the at least one gene in the manner associated with activation of the progesterone receptor as set forth in (ii) but not (i), indicates that the putative agonist ligand is a PR-B-specific agonist.

Another embodiment of the present invention relates to a method to identify isoform-specific antagonists of progesterone receptors, comprising: (a) contacting a progesterone receptor with a putative antagonist ligand, wherein the progesterone receptor is selected from the group consisting of progesterone receptor A (PR-A) and progesterone receptor B (PR-B), under conditions wherein, in the absence of the putative antagonist ligand, the progesterone receptor is activated; (b) detecting expression of at least one gene that is regulated by the progesterone receptor when the progesterone receptor is activated; and (c) comparing the expression of the at least one gene in the presence and in the absence of the putative antagonist ligand. In this embodiment, the at least one gene is selected from the group consisting of: (i) at least one gene that is exclusively upregulated or downregulated by PR-A, chosen from a Table selected from the group consisting of Table 1 and Table 2; and, (ii) at least one gene that is exclusively upregulated or downregulated by PR-B chosen from a Table selected from the group consisting of Table 3 and Table 4. In the presence of the putative antagonist ligand, detection of inhibition or reversal of the regulation of expression of the at least one gene as compared to the regulation of expression of the at least one gene in the manner associated with activation of the progesterone receptor as set forth in (i) but not (ii), indicates that the putative antagonist ligand is a PR-A-specific antagonist, and wherein, in the presence of the putative antagonist ligand, detection of inhibition or reversal of the regulation of expression of the at least one gene as compared to the regulation of the expression of the at least one gene in the manner associated with activation of the

progesterone receptor as set forth in (ii) but not (i), indicates that the putative antagonist ligand is a PR-B-specific antagonist.

Given the knowledge of the genes regulated exclusively by progesterone receptor isoforms according to the present invention, one of skill in the art will be able to select one or more genes to detect in a method of the present invention, and the selection of the one or more genes can be determined by different factors. For example, one of skill in the art may wish to further select genes to be detected on the basis of the function of the gene or gene product, on the basis of tissue-type in which a PR is expressed, on the basis of association with a particular condition or disease, or on the basis of the change in the level of expression of the gene when in the presence of progesterone. Such embodiments have generally been described above.

Antiprogestins that selectively inhibit progestin effects on only one of the two PRs, would be highly desirable, but do not exist at present. Such antagonist ligands would be useful not only for breast cancer treatment, but to treat a variety of reproductive disorders, and for contraception. Antagonists that can inhibit only PR-A without affecting PR-B (and *vice-versa*) would be highly desirable. The current invention allows for rapid and direct screening for such ligands. For example, the invention identifies clusters of genes that are upregulated only by PR-A or PR-B in the presence of the agonist, progesterone. These gene clusters are perfect targets for antiprogestin (antagonist) and progestin (agonist) screening by the cell-free *in vitro*, intact cell *in vitro*, or whole animal endogenous or transgenic methods described above. For the embodiment related to antagonists, a selected cluster of one, two or more of the genes of this invention that are exclusively regulated by PR-A or PR-B would first be activated by progesterone or another progestin. Putative antiprogestins would be screened and selected on the basis of their ability to reverse or inhibit the effects of the agonist, progesterone, by comparing the expression profiles of the genes in the presence of the putative antiprogestin to the expression profile of the genes as a result of activation of the receptor with a progestin. Isoform-specific agonists of PRs can be similarly selected by choosing ligands on the basis of their ability to mimic the effects of the agonist, progesterone, on the PR isoforms.

These two embodiments of the present invention take advantage of the knowledge provided herein of the isoform-specific regulation of genes by progesterone receptors. Prior to the present invention, such assays were impossible, because the specific regulation of a gene by one PR isoform, and not the other, was not known. By way of example, if a gene in Table 1 is detected (i.e., a gene that is known to be upregulated selectively (i.e., exclusively, uniquely) by PR-A) when the PR to be tested (at least PR-A or a combination of PR-A and PR-B) is in the presence of a putative regulatory ligand, and the expression of that gene is determined to be in the manner associated with activation of the progesterone receptor (i.e., the gene is upregulated), then it can be concluded that the putative regulatory compound is a PR-A-specific agonist, because the present inventors have shown that the gene is exclusively upregulated by PR-A. Similarly, if a gene in Table 4 is detected (i.e., a gene that is known to be downregulated selectively (i.e., exclusively, uniquely) by PR-B) when the PR to be tested (at least PR-B or a combination of PR-A and PR-B) is in the presence of a putative regulatory ligand, and the expression of that gene is determined to be in the manner associated with activation of the progesterone receptor (i.e., the gene is downregulated), then it can be concluded that the putative regulatory compound is a PR-B-specific agonist, because the present inventors have shown that this particular gene is exclusively downregulated by PR-B. For a putative antagonist, if the same gene in Table 4 is detected when the PR to be tested is or will be activated and is in the presence of the putative antagonist, and the expression of that gene is determined to be inhibited or reversed (i.e., the gene is upregulated or is statistically significantly less downregulated) as compared to the expression of the gene in the manner associated with activation of the progesterone receptor, then it can be concluded that the putative regulatory compound is a PR-B-specific antagonist, because the present inventors have shown that this particular gene is exclusively downregulated by PR-B.

The particular details relating to the contacting, detecting and comparing steps of the above-described methods for identification of PR isoform-specific ligands are substantially the same as those described above for the broader methods of identifying PR regulatory ligands and will not be repeated here.

Agonists and antagonists of progesterone receptors identified by the above methods or any other suitable method are useful in a variety of therapeutic methods as described herein.

Yet another embodiment of the present invention relates to a method to identify a tissue-specific agonist of a progesterone receptor. This method includes the steps of: (a) providing an expression profile for at least one gene that is known to be regulated by a progesterone receptor in both a first and second tissue type when the progesterone receptor is activated, wherein the at least one gene is chosen from the genes in any one or more of the genes in Tables 1-7; (b) contacting a progesterone receptor expressed by a first tissue type with a putative agonist ligand, wherein the progesterone receptor is selected from the group consisting of progesterone receptor A (PR-A) and progesterone receptor B (PR-B), under conditions wherein, in the absence of the putative agonist ligand, the progesterone receptor is not activated; (c) contacting a progesterone receptor expressed by a second tissue type with the putative agonist ligand under conditions wherein, in the absence of the putative agonist ligand, the progesterone receptor is not activated, wherein the progesterone receptor is the same isoform as the progesterone receptor contacted in (b); (d) detecting expression of the at least one gene from (a); and, (e) comparing the expression of the at least one gene in the presence and in the absence of the putative agonist ligand in each of the first and second tissue types. Detection of regulation of the expression of the at least one gene in one of the first or second tissue types in the manner associated with activation of the progesterone receptor as set forth in the expression profile of (a), and detection of inhibition of regulation or no regulation of the at least one gene in the other of the first or second tissue types, as compared to the expression of the at least one gene associated with activation of the progesterone receptor as set forth in the expression profile of (a), indicates that the putative agonist ligand is a tissue-specific progesterone receptor agonist.

Similarly, another embodiment of the present invention relates to a method to identify a tissue-specific agonist of a progesterone receptor, such method comprising: (a) providing an expression profile for at least one gene that is known to be regulated by a progesterone receptor in a first tissue type but not a second tissue type when the progesterone receptor is activated, wherein the at least one gene is chosen from the genes in any one or more of the

genes in Tables 1-7; (b) contacting a progesterone receptor expressed by the first tissue type with a putative agonist ligand, wherein the progesterone receptor is selected from the group consisting of progesterone receptor A (PR-A) and progesterone receptor B (PR-B), under conditions wherein, in the absence of the putative agonist ligand, the progesterone receptor is not activated; (c) detecting expression of the at least one gene from (a); (d) comparing the expression of the at least one gene in the presence and in the absence of the putative agonist ligand in the first tissue type, wherein detection of regulation of the expression of the at least one gene in the first tissue type in the manner associated with activation of the progesterone receptor as set forth in the expression profile of (a) indicates that the putative agonist ligand is a tissue-specific progesterone receptor agonist for the first tissue type. In this embodiment, it is desirable to include additional controls or the detection of multiple genes that confirm that the regulation of the PR by the putative regulatory ligand is tissue-specific.

Another embodiment of the present invention relates to a method to identify a tissue-specific antagonist of a progesterone receptor. This method includes the steps of: (a) providing an expression profile for at least one gene that is known to be regulated by a progesterone receptor in both a first and second tissue type when the progesterone receptor is activated, wherein the at least one gene is chosen from the genes in any one or more of the genes in Tables 1-7; (b) contacting a progesterone receptor expressed by a first tissue type with a putative antagonist ligand, wherein the progesterone receptor is selected from the group consisting of progesterone receptor A (PR-A) and progesterone receptor B (PR-B), under conditions wherein, in the absence of the putative antagonist ligand, the progesterone receptor is activated; (c) contacting a progesterone receptor expressed by a second tissue type with the putative antagonist ligand, wherein the progesterone receptor is selected from the group consisting of progesterone receptor A (PR-A) and progesterone receptor B (PR-B), under conditions wherein, in the absence of the putative antagonist ligand, the progesterone receptor is activated; (d) detecting expression of the at least one gene from (a); and, (e) comparing the expression of the at least one gene in the presence and in the absence of the putative antagonist ligand in each of the first and second tissue types, wherein detection of regulation of the expression of the at least one gene in one of the first or second tissue types in the manner associated with activation of the progesterone receptor as set forth in the

expression profile of (a) in the presence of the putative antagonist ligand, and detection of inhibition or reversal of regulation of expression of the at least one gene in the other of the first or second tissue types in the presence of the putative antagonist ligand, as compared to the expression of the at least one gene associated with activation of the progesterone receptor as set forth in the expression profile of (a), indicates that the putative antagonist ligand is a tissue-specific progesterone receptor antagonist.

Similarly, another embodiment of the present invention relates to a method to identify a tissue-specific antagonist of a progesterone receptor, such method including the steps of: (a) providing an expression profile for at least one gene that is known to be regulated by a progesterone receptor in a first but not in a second tissue type when the progesterone receptor is activated, wherein the at least one gene is chosen from the genes in any one or more of the genes in Tables 1-7; (b) contacting a progesterone receptor expressed by a first tissue type with a putative antagonist ligand, wherein the progesterone receptor is selected from the group consisting of progesterone receptor A (PR-A) and progesterone receptor B (PR-B), under conditions wherein, in the absence of the putative antagonist ligand, the progesterone receptor is activated; (c) detecting expression of the at least one gene from (a); and, (d) comparing the expression of the at least one gene in the presence and in the absence of the putative antagonist ligand in the first tissue type, wherein detection of inhibition or reversal of regulation of expression of the at least one gene in the first tissue type in the presence of the putative antagonist ligand, as compared to the expression of the at least one gene associated with activation of the progesterone receptor as set forth in the expression profile of (a), indicates that the putative antagonist ligand is a tissue-specific progesterone receptor antagonist of the first tissue type. In this embodiment, it is desirable to include additional controls or the detection of multiple genes that confirm that the regulation of the PR by the putative regulatory ligand is tissue-specific.

In one aspect of any of the above-described embodiments for identifying a tissue-specific regulator of PR activity, the first tissue type is breast, and at least one gene is selected from the group consisting of any one or more of the genes in Tables 1-7. In general, the first or second tissue type can be any tissue type, including any cell type, that expresses a progesterone receptor. For example, tissues that are known to express progesterone

receptors include, but are not limited to, breast, uterus, bone, cartilage, cardiovascular tissues, heart, lung, brain, meninges, pituitary, ovary, oocyte, corpus luteum, oviduct, fallopian tubes, T lymphocytes, B lymphocytes, thymocytes, salivary gland, placenta, skin, gut, pancreas, liver, testis, epididymis, bladder, urinary tract, eye, and teeth.

In another aspect, the first tissue type is a non-malignant tissue and wherein the second tissue type is a malignant tissue from the same tissue source as the first tissue type. A preferred tissue source for screening for regulators of malignant tissue but not non-malignant tissue is breast tissue.

In another aspect, the first tissue type is a normal tissue and wherein the second tissue type is a non-malignant, abnormal tissue. Such tissues include, but are not limited to, tissues from endometriosis and leiomyoma of the uterus, fibrocystic disease of the breast, or polycystic ovary.

In one aspect of the tissue-specific methods of the present invention, the method includes the detection of the any one or more of the following genes: 11-beta-hydroxysteroid dehydrogenase type 2, tissue factor gene, PCI gene (plasminogen activator inhibitor 3), MAD-3 Ikβ-alpha, Niemann-Pick C disease (NPC1), platelet-type phosphofructokinase, phenylethanolamine n-methyltransferase (PNMT), transforming growth factor-beta 3 (TGF-beta3), Monocyte Chemotactic Protein 1, delta sleep inducing peptide (related to TSC-22), estrogen receptor-related protein (hERRa1). These genes are of particular interest when one of the tissue types is the endometrium.

In another aspect of the tissue-specific methods of the present invention, the method includes the detection of the any one or more of the following genes: growth arrest-specific protein (gas6), tissue factor gene, NF-IL6-beta (C/EBPbeta), PCI gene (plasminogen activator inhibitor), Stat5A, calcium-binding protein S100P, MSX-2, lipocortin II (calpactin I), selenium-binding protein (hSBP), and bullous pemphigoid antigen (plakin family). These genes are of particular interest when one of the tissue types is the breast.

In another aspect of the tissue-specific methods of the present invention, the method includes the detection of phenylethanolamine n-methyltransferase (PNMT) adrenal medulla. This gene is of particular interest when one of the tissue types is brain tissue.

In another aspect of the tissue-specific methods of the present invention, the method includes the detection of proteasome-like subunit MECL-1. This gene is of particular interest when one of the tissue types is thymus tissue.

In yet another aspect of these methods, the expression profile of genes regulated by a progesterone receptor in the first or second tissue type is provided by a method comprising: (a) providing a first cell of a selected tissue type that expresses a progesterone receptor A (PR-A) and not a progesterone receptor B (PR-B) and a second cell of the same tissue type that expresses PR-B and not PR-A; (b)stimulating the progesterone receptors in (a) by contacting the first and second cells with a progesterone receptor stimulatory ligand; (c) detecting expression of genes by the first and second cells in the presence of the stimulatory ligand and in the absence of the stimulatory ligand, wherein a difference in the expression of a gene in the presence of the stimulatory ligand as compared to in the absence of the stimulatory ligand, indicates that the gene is regulated by the progesterone receptor in the selected tissue type.

The present invention defines genes that are regulated by PR-A *vs.* PR-B in breast cancer cells. It is believed that many, if not most of these genes, will also be regulated by progesterone receptors in other tissues. Similar data can be generated for other tissues, including the uterus, bone, cardiovascular tissues, etc., or malignant *vs.* normal tissues. Progestin regulated genes in other tissues, which differ from the genes in breast cancer cells of this invention, can be identified, and be used to screen for ligands that regulate candidate genes only in the desired tissue. For example, using the appropriate gene clusters, one could identify a ligand that activates PR-A in the uterus but not the breast. Similarly one could screen out ligands that have undesirable organ or tissue effects. For example, ligands that are inadvertently bioactive in the liver, where they might induce liver toxicity, could be discarded. Alternatively, when a gene is regulated in both tissue types, one can screen for ligands that regulate the expression of the gene in one tissue type, but not the other tissue type. For example, by using tissue specific methods described above, it is also possible to screen for antagonists that block the actions of progestins in one organ or tissue and through one PR isoform, but not another organ or tissue and the other PR isoform. For example, if

PR-A are "good" receptors in the uterus but not the breast, a selective "antiprogestin-A" might be found that is only inhibitory in the breast.

Given the guidance provided herein, it is within the ability of those of skill in the art to screen other tissue types for the presence or absence of the genes regulated by PR in breast tissue, and/or to perform a *de novo* screening assay for the identification of genes regulated by PR in another tissue, to develop gene expression profiles for use in screening for tissue specific ligands. One of skill in the art can now look to see if a given gene that is regulated by PR in breast is also regulated by PR in another tissue type, thereby providing a gene profile for use in the tissue-specific ligand identification methods of the present invention.

The particular details relating to the contacting, detecting and comparing steps of the above-described methods for identification of PR isoform-specific ligands are substantially the same as those described above for the broader methods of identifying PR regulatory ligands and will not be repeated here.

Another method of the present invention relates to a method to identify genes that are regulated by a progesterone receptor in two or more tissue types. The method includes the steps of: (a) activating a progesterone receptor in two or more tissue types that express the progesterone receptor; (b) detecting expression of at least one gene in the two or more tissue types, the at least one gene being chosen from a gene in any one or more of Tables 1-7, and, (c) identifying genes that are regulated by the progesterone receptor in each of the two or more tissue types. In one embodiment, the method further includes detecting whether the genes are regulated selectively by PR-A, selectively by PR-B, or by both PR-A and PR-B. This method can generally be used to provide a profile of genes in a tissue type other than breast. Such a profile can then be used in a method for the identification of tissue-specific progesterone receptor ligands as described above, or in a method of determining a profile of genes for a given tissue sample as described below.

Yet another embodiment of the present invention relates to a method to determine the profile of genes regulated by progesterone receptors in a tissue sample. In a preferred embodiment, the sample is a breast tumor sample. This method includes the steps of: (a) obtaining from a patient a breast tumor sample; (b) detecting expression of at least one gene in the breast tumor sample that is regulated by a progesterone receptor when the progesterone

receptor is activated; and, (c) producing a profile of genes for the tumor sample that are regulated selectively by PR-A, selectively by PR-B, or by both PR-A and PR-B. In this embodiment, the gene(s) to be profiled are being selected from the group consisting of: (i) at least one gene that is selectively upregulated by PR-A chosen from a gene in Table 9; (ii) at least one gene that is selectively downregulated by PR-A chosen from a gene in Table 10; (iii) at least one gene that is selectively upregulated by PR-B chosen from a gene in Table 11; (iv) at least one gene that is selectively downregulated by PR-B chosen from a gene in Table 12; (v) at least one gene that is upregulated or downregulated by both PR-A and PR-B chosen from a gene in Table 13; (vi) at least one gene that is reciprocally regulated by PR-A and PR-B chosen from a gene in Table 14; and, (vii) at least one gene that is regulated by one of the PR-A or the PR-B, wherein regulation of the gene is altered when the other of the PR-A or PR-B is expressed by the same cell, chosen from a gene in Table 15.

Because of their physiological importance in the breast, PRs are routinely measured in all breast cancers when the disease is first diagnosed. Presence of PRs, especially if the levels are high, informs the oncologist that the tumor is likely to be "hormone-dependent" and will respond to endocrine treatments. This spares the woman from much harsher treatments involving chemotherapies. Additionally, the number of PRs allows the oncologist to predict how aggressive the tumor is likely to be. High PR levels in her tumor indicates that a woman's prognosis is good. Thus measurement of total PRs levels plays a key role in the management of breast cancers.

Both PR-A and PR-B are present in PR-positive breast cancers. The PR-A:PR-B ratio varies widely from tumor to tumor, and some tumors express only one or the other isoform. However, the clinical consequences of this heterogeneity are unknown. Because the transcriptional effects of the two PRs are believed to be so different, fluctuations in their ratio are expected to critically influence the biology of the tumors. However, at present, how that biology is affected is unknown. Whether in fact, PR-A are "bad" and PR-B are "good" in breast cancers, is also unknown. Since most breast cancer cell lines lose their PRs, and both isoforms are co-expressed in cell lines that retain their PRs, one way to determine the biological consequences of varying A:B ratios is to define the endogenous genes that each of the two PRs regulates independently. Knowledge of the unique sets of genes that are

selectively regulated by each PR isoform as disclosed herein allows the genes to serve as surrogate markers for the presence and function of PR-A *vs.* PR-B. Furthermore, knowledge of such genes and their promoters, allows the genes to serve as a tool for screening PR-A vs. PR-B selective ligands. However, prior to the present invention, defining which sets of genes were uniquely regulated by one or the other PR in breast cancers was impossible because both receptors are simultaneously activated by progesterone treatment. The present invention has provided a solution to this problem.

As discussed above, total PRs are routinely measured in all primary breast cancers as a guide to therapy. Their presence and levels are used to predict whether the tumor is likely to respond to hormone treatments, and to estimate disease prognosis. Tumors that lack PRs have less than 10% chance of responding to hormone treatments; tumors that contain PRs have on average a 70% chance of responding to hormone treatments depending on the receptor levels. These numbers are statistical only, and therefore are not specifically informative for any individual patient. The present invention has led to the development of assays that profile the tumor of an individual patient for "good" and "bad" surrogate markers of PR-A and PR-B. Thus it is now possible to measure not only the presence of PRs in a tumor, but the function of the PRs in that tumor.

In this embodiment, one or more of the genes set forth in Tables 9-15 are selected to be screened in a tissue sample from a patient. Preferably, the tissue sample is a breast tumor sample. The expression of the genes in the tissue sample can be detected using techniques described above for the various other methods of the present invention. For example, transcript expression levels of the selected genes can be measured in the tumor of a patient, by any of a number of known methods. For mRNA expression, methods include but are not limited to: northern blotting; reverse transcriptase - polymerase chain reaction and detection of the product; use of labeled mRNA from the tumor to probe cDNAs or oligonucleotides encoding all or part of the PR-responsive genes of interest, arrayed on any of a variety of surfaces, as described above. For detection of protein expression levels of the selected genes, methods include but are not limited to: western blotting, immunocytochemistry, flow cytometry or other immunologic-based assays; assays based on a property of the protein including but not limited to DNA binding, ligand binding, or interaction with other protein

partners, as described above. The presence and quantity of each gene marker can be measured in primary tumors, metastatic tumors, locally recurring tumors, ductal carcinomas in situ, or other tumors of breast cell origin. The markers can be measured in solid tumors that are fresh, frozen, fixed or otherwise preserved. They can be measured in cytoplasmic or nuclear tumor extracts; or in tumor membranes including but not limited to plasma, mitochondrial, golgi or nuclear membranes; in the nuclear matrix; or in tumor cell organelles and their extracts including but not limited to ribosomes, nuclei, mitochondria, golgi.

A profile of individual gene markers, including a matrix of two or more markers, can be generated by one or more of the methods described above. According to the present invention, a profile of the genes regulated by progesterone receptors in a tissue sample refers to a reporting of the expression level of a given gene from Tables 9-15, wherein, based on the knowledge of the regulation of the genes provided by Tables 9-15, includes a classification of the gene with regard to how the gene is regulated by the PR isoforms. For example, if the gene, estrogen receptor-related protein, is identified as being expressed by a tumor sample, the profile for the tumor will include the reporting of the expression of at least one gene that is exclusively regulated by PR-A. The data can be reported as raw data, and/or statistically analyzed by any of a variety of methods, and/or combined with any other prognostic marker(s) including but not limited to ER, % S-phase, other proliferation markers, markers of ER expression, tumor suppressor genes, etc. Prior to the present invention, one of skill in the art would not have known to screen breast tumors for the genes in Tables 1-7, 9-10 or 18-19, (excepting genes in Table 16), and one of skill in the art would not have been able to classify any of these genes on the basis of the PR isoform regulation.

Given the knowledge of the genes regulated by progesterone receptor isoforms according to the present invention, one of skill in the art will be able to select one or more genes to detect in this method of the present invention, and the selection of the one or more genes can be determined by different factors. For example, one of skill in the art may wish to further select genes to be detected on the basis of the function of the gene or gene product, on the basis of PR isoform-specificity, on the basis of association with a particular condition or disease, or on the basis of the change in the level of expression of the gene when in the presence of progesterone. Such embodiments have generally been described above.

In one aspect of this method of the present invention, the method preferably includes the detection of the any one or more of the following genes: growth arrest-specific protein (gas6), tissue factor gene, NF-IL6-beta (C/EBPbeta), PCI gene (plasminogen activator inhibitor), Stat5A, calcium-binding protein S100P, MSX-2, lipocortin II (calpactin I), selenium-binding protein (hSBP), and bullous pemphigoid antigen (plakin family). These genes are of particular interest when one of the tissue types is the breast.

In another aspect of this method of the present invention, the method preferably includes the detection of the any one of more of the following genes: growth arrest-specific protein (gas6), NF-IL6-beta (C/EBPbeta), calcium-binding protein S100P, MSX-2, selenium-binding protein (hSBP), and bullous pemphigoid antigen (plakin family).

The profile of genes provided as a result of the screening of the tissue can be used by the patient or physician for decision-making regarding the usefulness of endocrine therapies in general (i.e. oophorectomy, antiestrogens or other SERMs, aromatase inhibitors, or others), or progestational therapy in particular (high dose progestins, antiprogestins or others). The profile can be used to estimate how the disease is likely to respond and progress in any individual patient. Clinical trials can be developed to correlate the relationship between PR-A *vs.* PR-B regulated genes, and the biological behavior of the tumor.

In addition, if it is determined that one PR isoform is harmful, and the other beneficial, the gene clusters of this invention can be measured or quantified in normal breast or other normal tissues, either frozen or preserved, or in tissue or organelle extracts as described above, either alone or together with other markers (for example BRCA1), and used for genetic counseling.

In addition, one of the key questions that the present invention can address, is whether breast tumors that overexpress PR-B or PR-A represent phenotypically different tumor subsets. For example, breast tumors that are identified as "PR-B rich" based on their expression of PR-B specific genes, can be further assessed in terms of usual clinical parameters -- tumor staging, pathological staging, size, nodal status, metastasis, responsiveness to hormonal and chemotherapies -- and compared to parallel tumors that are "PR-A rich". Without being bound by theory, the present inventors predict that PR-B rich tumors may be larger and more aggressive than PR-A rich tumors. One reason for this is that

this invention demonstrates that PR-B strongly and uniquely upregulate two important genes that support angiogenesis: L13720, growth arrest-specific protein (gas 6) is increased 23.1 fold; M27436, tissue factor gene is increased 18.1 fold. Increased angiogenesis, by increasing their blood (and nutrient) supply, promotes tumor growth. This is one example of the hypotheses that can be raised and tested, based on the new information revealed by this invention.

In one aspect of this embodiment of the invention, the profiling of genes can be extended to other tissue types and/or other genes. For example, as discussed above, using the guidance provided herein, it is within the ability of those of skill in the art to screen other tissue types for the presence or absence of the genes regulated by PR in breast tissue, and/or to perform a de novo screening assay for the identification of genes regulated by PR in another tissue, to develop gene expression profiles for use in screening for tissue specific ligands. One of skill in the art can now look to see if a given gene that is regulated by PR in breast is also regulated by PR in another tissue type. Moreover, the 4 breast cancer cell lines described in Example 1, can be used to screen other gene arrays, including arrays of expressed tag sequences, to discover additional novel, PR-A *vs.* PR-B regulated genes. The procedure used to produce these cells can be extended to cells from other tissue sources (e.g., the uterus), and new PR-A and PR-B regulated genes can be identified for these tissue sources. Additional applications of the present invention include screening for genes that are regulated by PRs in a ligand-independent manner. The extension of the gene profiles to other tissue types will allow for the development of a variety of diagnostic assays in other tissues and for diseases related to such other tissues, as well as the identification of additional targets for therapeutic strategies.

Another embodiment of the present invention relates to a plurality of polynucleotides for the detection of the expression of genes regulated by progesterone receptors in breast tissue. The plurality of polynucleotides consists of polynucleotide probes that are complementary to RNA transcripts, or nucleotides derived therefrom, of genes that are regulated by progesterone receptors, and is therefore distinguished from previously known nucleic acid arrays and primer sets. The plurality of polynucleotides within the above-limitation includes at least one or more, but is not limited to one or more, polynucleotide

probes that are complementary to RNA transcripts, or nucleotides derived therefrom, of genes identified by the present inventors. Such genes are selected from: (a) at least one gene that is selectively upregulated by PR-A chosen from a gene in Table 1; (b) at least one gene that is selectively downregulated by PR-A chosen from a gene in Table 2; (c) at least one gene that is selectively upregulated by PR-B chosen from a gene in Table 3; (d) at least one gene that is selectively downregulated by PR-B chosen from a gene in Table 4; (e) at least one gene that is upregulated or downregulated by both PR-A and PR-B chosen from a gene in Table 5; (f) at least one gene that is reciprocally regulated by PR-A and PR-B chosen from a gene in Table 6; and, (g) at least one gene that is regulated by one of the PR-A or the PR-B, wherein regulation of the gene is altered when the other of the PR-A or PR-B is expressed by the same cell, chosen from a gene in Table 7.

In one embodiment, it is contemplated that additional genes that are not regulated by progesterone receptors can be added to the plurality of polynucleotides. Such genes would not be random genes, or large groups of unselected human genes, as are commercially available now, but rather, would be specifically selected to complement the sets of progesterone receptor-regulated genes identified by the present invention. For example, one of skill in the art may wish to add to the above-described plurality of genes one or more genes that are of relevance because they are expressed by a particular tissue of interest (e.g., breast tissue), are associated with a particular disease or condition of interest (e.g., breast cancer), or are associated with a particular cell, tissue or body function (e.g., angiogenesis). The development of additional pluralities of polynucleotides (and antibodies, as disclosed below), which include both the above-described plurality and such additional selected polynucleotides, are explicitly contemplated by the present invention.

In one embodiment, the plurality of polynucleotides further comprises at least one polynucleotide probe that is complementary to RNA transcripts, or nucleotides derived therefrom, of at least one gene chosen from the genes in Table 8. In another embodiment, the plurality of polynucleotides comprises polynucleotide probes that are complementary to RNA transcripts, or nucleotides derived therefrom, of particular subsets of the genes disclosed in the present invention. For example, one of skill in the art may wish to design pluralities of polynucleotides on the basis of the function of the gene or gene product, on the

basis of a tissue-type that expresses a PR, on the basis of PR isoform specificity, on the basis of association with a particular condition or disease, or on the basis of the change in the level of expression of the gene when in the presence of progesterone. Such embodiments have generally been described above.

According to the present invention, a plurality of polynucleotides refers to at least 2, and more preferably at least 3, and more preferably at least 4, and more preferably at least 5, and more preferably at least 6, and more preferably at least 7, and more preferably at least 8, and more preferably at least 9, and more preferably at least 10, and so on, in increments of one, up to any suitable number of polynucleotides, including at least 100, 500, 1000, 10^4, 10^5, or at least 10^6 or more polynucleotides.

In accordance with the present invention, an isolated polynucleotide, or an isolated nucleic acid molecule, is a nucleic acid molecule that has been removed from its natural milieu (i.e., that has been subject to human manipulation), its natural milieu being the genome or chromosome in which the nucleic acid molecule is found in nature. As such, "isolated" does not necessarily reflect the extent to which the nucleic acid molecule has been purified, but indicates that the molecule does not include an entire genome or an entire chromosome in which the nucleic acid molecule is found in nature. The polynucleotides useful in the plurality of polynucleotides of the present invention are typically a portion of a gene of the present invention that is suitable for use as a hybridization probe or PCR primer for the identification of a full-length gene (or portion thereof) in a given sample (e.g., a cell sample). An isolated nucleic acid molecules can include a gene or a portion of a gene (e.g., the regulatory region or promoter), for example, to produce a reporter construct according to the present invention. An isolated nucleic acid molecule that includes a gene is not a fragment of a chromosome that includes such gene, but rather includes the coding region and regulatory regions associated with the gene, but no additional genes naturally found on the same chromosome. An isolated nucleic acid molecule can also include a specified nucleic acid sequence flanked by (i.e., at the 5' and/or the 3' end of the sequence) additional nucleic acids that do not normally flank the specified nucleic acid sequence in nature (i.e., heterologous sequences). Isolated nucleic acid molecule can include DNA, RNA (e.g., mRNA), or derivatives of either DNA or RNA (e.g., cDNA). Although the phrase "nucleic

acid molecule" primarily refers to the physical nucleic acid molecule and the phrase "nucleic acid sequence" primarily refers to the sequence of nucleotides on the nucleic acid molecule, the two phrases can be used interchangeably, especially with respect to a nucleic acid molecule, or a nucleic acid sequence, being capable of encoding a protein. Preferably, an isolated nucleic acid molecule of the present invention is produced using recombinant DNA technology (e.g., polymerase chain reaction (PCR) amplification, cloning) or chemical synthesis. If the polynucleotide is an oligonucleotide probe, the probe preferably ranges from about 5 to about 50 or about 500 nucleotides, more preferably from about 10 to about 40 nucleotides, and most preferably from about 15 to about 40 nucleotides in length.

In one embodiment, the polynucleotide probes are conjugated to detectable markers. Detectable labels suitable for use in the present invention include any composition detectable by spectroscopic, photochemical, biochemical, immunochemical, electrical, optical or chemical means. Useful labels in the present invention include biotin for staining with labeled streptavidin conjugate, magnetic beads (e.g., Dynabeads.TM.), fluorescent dyes (e.g., fluorescein, texas red, rhodamine, green fluorescent protein, and the like), radiolabels (e.g., ^{3}H, ^{125}I, ^{35}S, ^{14}C, or ^{32}P), enzymes (e.g., horse radish peroxidase, alkaline phosphatase and others commonly used in an ELISA), and colorimetric labels such as colloidal gold or colored glass or plastic (e.g., polystyrene, polypropylene, latex, etc.) beads. Preferably, the polynucleotide probes are immobilized on a substrate.

In one embodiment, the polynucleotide probes are hybridizable array elements in a microarray or high density array. Nucleic acid arrays are well known in the art and are described for use in comparing expression levels of particular genes of interest, for example, in U.S. Patent No. 6,177,248, which is incorporated herein by reference in its entirety. Nucleic acid arrays are suitable for quantifying a small variations in expression levels of a gene in the presence of a large population of heterogeneous nucleic acids. Knowing the identity of the downstream genes of the present invention, nucleic acid arrays can be fabricated either by *de novo* synthesis on a substrate or by spotting or transporting nucleic acid sequences onto specific locations of substrate. Nucleic acids are purified and/or isolated from biological materials, such as a bacterial plasmid containing a cloned segment of sequence of interest. It is noted that all of the genes identified by the present invention have

been previously sequenced, at least in part, such that oligonucleotides suitable for the identification of such nucleic acids can be produced. The database accession number for each of the genes identified by the present inventors is provided in the tables of the invention. Suitable nucleic acids are also produced by amplification of template, such as by polymerase chain reaction or in vitro transcription.

Synthesized oligonucleotide arrays are particularly preferred for this aspect of the invention. Oligonucleotide arrays have numerous advantages, as opposed to other methods, such as efficiency of production, reduced intra- and inter array variability, increased information content and high signal-to-noise ratio.

One of skill in the art will appreciate that an enormous number of array designs are suitable for the practice of this invention. An array will typically include a number of probes that specifically hybridize to the sequences of interest. In addition, in a preferred embodiment, the array will include one or more control probes. The high-density array chip includes "test probes." Test probes could be oligonucleotides that range from about 5 to about 45 or 5 to about 500 nucleotides, more preferably from about 10 to about 40 nucleotides and most preferably from about 15 to about 40 nucleotides in length. In other particularly preferred embodiments the probes are 20 or 25 nucleotides in length. In another preferred embodiments, test probes are double or single strand DNA sequences. DNA sequences are isolated or cloned from natural sources or amplified from natural sources using natural nucleic acids as templates, or produced synthetically. These probes have sequences complementary to particular subsequences of the genes whose expression they are designed to detect. Thus, the test probes are capable of specifically hybridizing to the target nucleic acid they are to detect.

Another embodiment of the present invention relates to a plurality of antibodies, or antigen binding fragments thereof, for the detection of the expression of genes regulated by progesterone receptors in breast tissue. The plurality of antibodies, or antigen binding fragments thereof, consists of antibodies, or antigen binding fragments thereof, that selectively bind to proteins encoded by genes that are regulated by progesterone receptors. In addition, the plurality of antibodies, or antigen binding fragments thereof, comprises antibodies, or antigen binding fragments thereof, that selectively bind to proteins encoded

by genes selected from the group consisting of: (a) genes that are selectively upregulated by PR-A chosen from genes in Table 1; (b) genes that are selectively downregulated by PR-A chosen from genes in Table 2; (c) genes that are selectively upregulated by PR-B chosen from genes in Table 3; (d) genes that are selectively downregulated by PR-B chosen from genes in Table 4; (e) genes that are upregulated or downregulated by both PR-A and PR-B chosen from genes in Table 5; (f) genes that are reciprocally regulated by PR-A and PR-B chosen from genes in Table 6; and, (g) genes that are regulated by one of the PR-A or the PR-B, wherein regulation of the gene is altered when the other of the PR-A or PR-B is expressed by the same cell, chosen from genes in Table 7.

In one aspect, the plurality of antibodies, or antigen binding fragments thereof, further comprises at least one antibody, or an antigen binding fragment thereof, that selectively binds to a protein encoded by a gene chosen from the genes in Table 8.

The plurality of antibodies, or antigen binding fragments thereof, further comprises at least one antibody, or an antigen binding fragment thereof, that selectively binds to a protein encoded by a one or more of a particular subset of the genes disclosed in the present invention. For example, one of skill in the art may wish to design pluralities of antibodies on the basis of the function of the gene product, on the basis of tissue-type, on the basis of PR isoform specificity, on the basis of association with a particular condition or disease, or on the basis of the change in the level of expression of the gene when in the presence of progesterone. Such embodiments have generally been described above.

According to the present invention, a plurality of antibodies, or antigen binding fragments thereof, refers to at least 2, and more preferably at least 3, and more preferably at least 4, and more preferably at least 5, and more preferably at least 6, and more preferably at least 7, and more preferably at least 8, and more preferably at least 9, and more preferably at least 10, and so on, in increments of one, up to any suitable number of antibodies, or antigen binding fragments thereof, including at least 100, 500, or at least 1000 antibodies, or antigen binding fragments thereof.

According to the present invention, the phrase "selectively binds to" refers to the ability of an antibody, antigen binding fragment or binding partner of the present invention to preferentially bind to specified proteins (e.g., a protein encoded by a PR regulated gene

according to the present invention). The phrase "selectively binds" with regard to antibodies and antigen binding fragments thereof, has been defined previously herein.

Limited digestion of an immunoglobulin with a protease may produce two fragments. An antigen binding fragment is referred to as an Fab, an Fab', or an $F(ab')_2$ fragment. A fragment lacking the ability to bind to antigen is referred to as an Fc fragment. An Fab fragment comprises one arm of an immunoglobulin molecule containing a L chain ($V_L + C_L$ domains) paired with the V_H region and a portion of the C_H region (CH1 domain). An Fab' fragment corresponds to an Fab fragment with part of the hinge region attached to the CH1 domain. An $F(ab')_2$ fragment corresponds to two Fab' fragments that are normally covalently linked to each other through a di-sulfide bond, typically in the hinge regions.

Isolated antibodies of the present invention can include serum containing such antibodies, or antibodies that have been purified to varying degrees. Whole antibodies of the present invention can be polyclonal or monoclonal. Alternatively, functional equivalents of whole antibodies, such as antigen binding fragments in which one or more antibody domains are truncated or absent (e.g., Fv, Fab, Fab', or $F(ab)_2$ fragments), as well as genetically-engineered antibodies or antigen binding fragments thereof, including single chain antibodies or antibodies that can bind to more than one epitope (e.g., bi-specific antibodies), or antibodies that can bind to one or more different antigens (e.g., bi- or multi-specific antibodies), may also be employed in the invention.

Generally, in the production of an antibody, a suitable experimental animal, such as, for example, but not limited to, a rabbit, a sheep, a hamster, a guinea pig, a mouse, a rat, or a chicken, is exposed to an antigen against which an antibody is desired. Typically, an animal is immunized with an effective amount of antigen that is injected into the animal. An effective amount of antigen refers to an amount needed to induce antibody production by the animal. The animal's immune system is then allowed to respond over a pre-determined period of time. The immunization process can be repeated until the immune system is found to be producing antibodies to the antigen. In order to obtain polyclonal antibodies specific for the antigen, serum is collected from the animal that contains the desired antibodies (or in the case of a chicken, antibody can be collected from the eggs). Such serum is useful as

a reagent. Polyclonal antibodies can be further purified from the serum (or eggs) by, for example, treating the serum with ammonium sulfate.

Monoclonal antibodies may be produced according to the methodology of Kohler and Milstein (*Nature* 256:495-497, 1975). For example, B lymphocytes are recovered from the spleen (or any suitable tissue) of an immunized animal and then fused with myeloma cells to obtain a population of hybridoma cells capable of continual growth in suitable culture medium. Hybridomas producing the desired antibody are selected by testing the ability of the antibody produced by the hybridoma to bind to the desired antigen.

Finally, PR-regulated genes of this invention, or their RNA or protein products, can serve as targets for therapeutic strategies. For example, neutralizing antibodies could be directed against one of the protein products of a selected gene, expressed on the surface of a tumor cell.

One embodiment of this aspect of the invention relates to a method to regulate the expression of a gene selected from the group consisting of any one or more of the genes in Tables 1-7. The method includes administering to a cell that expresses a progesterone receptor a compound selected from the group consisting of: progesterone, a progestin, and an antiprogestin, wherein the compound is effective to regulate the expression of the gene(s) in Table 1-7. In a preferred embodiment, the gene is selected from the group consisting of genes that are listed in Table 16 (known to be involved in breast cancer or mammary gland development), but not in Table 8 (known to be regulated by progesterone). Such genes include, e.g., growth arrest-specific protein (gas6), NF-IL6-beta (C/EBPbeta), calcium-binding protein S100P, MSX-2, selenium-binding protein (hSBP), and bullous pemphigoid antigen (plakin family). In this aspect of the invention, the cell that expresses a progesterone receptor is in the breast tissue of a patient that has, or is at risk of developing, breast cancer. In addition to administering a progestin to the cell, these genes can serve as targets for the development of other therapeutic methods.

Once a suitable therapeutic compound, including a progesterone receptor agonist or antagonist, is identified using the methods and genes of the present invention, a composition can be formulated. A composition, and particularly a therapeutic composition, of the present invention generally includes the therapeutic compound (e.g., the progesterone receptor

regulatory ligand) and a carrier, and preferably, a pharmaceutically acceptable carrier. According to the present invention, a "pharmaceutically acceptable carrier" includes pharmaceutically acceptable excipients and/or pharmaceutically acceptable delivery vehicles, which are suitable for use in administration of the composition to a suitable *in vitro*, *ex vivo* or *in vivo* site. A suitable *in vitro*, *in vivo* or *ex vivo* site is preferably a cell that expresses a progesterone receptor. In some embodiments, a suitable site for delivery is a site of inflammation, a site of a tumor, a site of a transplanted graft, or a site of any other disease or condition in which progesterone receptor regulation, or modulation of genes regulated by a PR, can be beneficial, particularly given the knowledge of the genes regulated by PR according to the invention. Preferred pharmaceutically acceptable carriers are capable of maintaining a steroidal or non-steroidal compound, a protein, a peptide, nucleic acid molecule or mimetic (drug) according to the present invention in a form that, upon arrival of the steroidal or non-steroidal compound, protein, peptide, nucleic acid molecule or mimetic at the cell target in a culture or in patient, the steroidal or non-steroidal compound, protein, peptide, nucleic acid molecule or mimetic is capable of interacting with its target (e.g., a naturally occurring PR or a nucleic acid or protein product of a PR-regulated gene).

Suitable excipients of the present invention include excipients or formularies that transport or help transport, but do not specifically target a composition to a cell (also referred to herein as non-targeting carriers). Examples of pharmaceutically acceptable excipients include, but are not limited to water, phosphate buffered saline, Ringer's solution, dextrose solution, serum-containing solutions, Hank's solution, other aqueous physiologically balanced solutions, oils, esters and glycols. Aqueous carriers can contain suitable auxiliary substances required to approximate the physiological conditions of the recipient, for example, by enhancing chemical stability and isotonicity.

Suitable auxiliary substances include, for example, sodium acetate, sodium chloride, sodium lactate, potassium chloride, calcium chloride, and other substances used to produce phosphate buffer, Tris buffer, and bicarbonate buffer. Auxiliary substances can also include preservatives, such as thimerosal, m- or o-cresol, formalin and benzol alcohol. Compositions of the present invention can be sterilized by conventional methods and/or lyophilized.

One type of pharmaceutically acceptable carrier includes a controlled release formulation that is capable of slowly releasing a composition of the present invention into a patient or culture. As used herein, a controlled release formulation comprises a compound of the present invention (e.g., a protein (including homologues), a drug, an antibody, a nucleic acid molecule, or a mimetic) in a controlled release vehicle. Suitable controlled release vehicles include, but are not limited to, biocompatible polymers, other polymeric matrices, capsules, microcapsules, microparticles, bolus preparations, osmotic pumps, diffusion devices, liposomes, lipospheres, and transdermal delivery systems. Other carriers of the present invention include liquids that, upon administration to a patient, form a solid or a gel *in situ*. Preferred carriers are also biodegradable (i.e., bioerodible). When the compound is a recombinant nucleic acid molecule, suitable delivery vehicles include, but are not limited to liposomes, viral vectors or other delivery vehicles, including ribozymes. Natural lipid-containing delivery vehicles include cells and cellular membranes. Artificial lipid-containing delivery vehicles include liposomes and micelles. A delivery vehicle of the present invention can be modified to target to a particular site in a patient, thereby targeting and making use of a compound of the present invention at that site. Suitable modifications include manipulating the chemical formula of the lipid portion of the delivery vehicle and/or introducing into the vehicle a targeting agent capable of specifically targeting a delivery vehicle to a preferred site, for example, a preferred cell type. Other suitable delivery vehicles include gold particles, poly-L-lysine/DNA-molecular conjugates, and artificial chromosomes.

A pharmaceutically acceptable carrier which is capable of targeting is herein referred to as a "delivery vehicle." Delivery vehicles of the present invention are capable of delivering a composition of the present invention to a target site in a patient. A "target site" refers to a site in a patient to which one desires to deliver a composition. For example, a target site can be any cell which is targeted by direct injection or delivery using liposomes, viral vectors or other delivery vehicles, including ribozymes and antibodies. Examples of delivery vehicles include, but are not limited to, artificial and natural lipid-containing delivery vehicles, viral vectors, and ribozymes. Natural lipid-containing delivery vehicles include cells and cellular membranes. Artificial lipid-containing delivery vehicles include

liposomes and micelles. A delivery vehicle of the present invention can be modified to target to a particular site in a subject, thereby targeting and making use of a compound of the present invention at that site. Suitable modifications include manipulating the chemical formula of the lipid portion of the delivery vehicle and/or introducing into the vehicle a compound capable of specifically targeting a delivery vehicle to a preferred site, for example, a preferred cell type. Specifically, targeting refers to causing a delivery vehicle to bind to a particular cell by the interaction of the compound in the vehicle to a molecule on the surface of the cell. Suitable targeting compounds include ligands capable of selectively (i.e., specifically) binding another molecule at a particular site. Examples of such ligands include antibodies, antigens, receptors and receptor ligands. Manipulating the chemical formula of the lipid portion of the delivery vehicle can modulate the extracellular or intracellular targeting of the delivery vehicle. For example, a chemical can be added to the lipid formula of a liposome that alters the charge of the lipid bilayer of the liposome so that the liposome fuses with particular cells having particular charge characteristics.

One preferred delivery vehicle of the present invention is a liposome. A liposome is capable of remaining stable in an animal for a sufficient amount of time to deliver a nucleic acid molecule (e.g., an anti-sense nucleic acid molecule that hybridizes to a nucleic acid sequence in a gene for which inhibition is desired) to a preferred site in the animal. A liposome, according to the present invention, comprises a lipid composition that is capable of delivering a nucleic acid molecule described in the present invention to a particular, or selected, site in a patient. A liposome according to the present invention comprises a lipid composition that is capable of fusing with the plasma membrane of the targeted cell to deliver a nucleic acid molecule into a cell. Suitable liposomes for use with the present invention include any liposome. Preferred liposomes of the present invention include those liposomes commonly used in, for example, gene delivery methods known to those of skill in the art. More preferred liposomes comprise liposomes having a polycationic lipid composition and/or liposomes having a cholesterol backbone conjugated to polyethylene glycol. Complexing a liposome with a nucleic acid molecule of the present invention can be achieved using methods standard in the art.

A liposome delivery vehicle is preferably capable of remaining stable in a patient for a sufficient amount of time to deliver a nucleic acid molecule or other compound of the present invention to a preferred site in the patient (i.e., a target cell). A liposome delivery vehicle of the present invention is preferably stable in the patient into which it has been administered for at least about 30 minutes, more preferably for at least about 1 hour and even more preferably for at least about 24 hours. A preferred liposome delivery vehicle of the present invention is from about 0.01 microns to about 1 microns in size.

Another preferred delivery vehicle comprises a viral vector. A viral vector includes an isolated nucleic acid molecule useful in the present invention, in which the nucleic acid molecules are packaged in a viral coat that allows entrance of DNA into a cell. A number of viral vectors can be used, including, but not limited to, those based on alphaviruses, poxviruses, adenoviruses, herpesviruses, lentiviruses, adeno-associated viruses and retroviruses.

A composition which includes an agonist or antagonist of a progesterone receptor can be delivered to a cell culture or patient by any suitable method. Selection of such a method will vary with the type of compound being administered or delivered (i.e., steroidal or non-steroidal compound, protein, peptide, nucleic acid molecule, or mimetic), the mode of delivery (i.e., *in vitro*, *in vivo*, *ex vivo*) and the goal to be achieved by administration/delivery of the compound or composition. According to the present invention, an effective administration protocol (i.e., administering a composition in an effective manner) comprises suitable dose parameters and modes of administration that result in delivery of a composition to a desired site (i.e., to a desired cell) and/or in the desired regulatory event (e.g., regulation of the PR receptor biological activity or of the biological activity of a gene that is regulated by PR).

Administration routes include *in vivo*, *in vitro* and *ex vivo* routes. *In vivo* routes include, but are not limited to, oral, nasal, intratracheal injection, inhaled, transdermal, rectal, and parenteral routes. Preferred parenteral routes can include, but are not limited to, subcutaneous, intradermal, intravenous, intramuscular and intraperitoneal routes. Intravenous, intraperitoneal, intradermal, subcutaneous and intramuscular administrations can be performed using methods standard in the art. Aerosol (inhalation) delivery can also

be performed using methods standard in the art (see, for example, Stribling et al., *Proc. Natl. Acad. Sci. USA* 189:11277-11281, 1992, which is incorporated herein by reference in its entirety). Oral delivery can be performed by complexing a therapeutic composition of the present invention to a carrier capable of withstanding degradation by digestive enzymes in the gut of an animal. Examples of such carriers, include plastic capsules or tablets, such as those known in the art. Direct injection techniques are particularly useful for suppressing graft rejection by, for example, injecting the composition into the transplanted tissue, or for site-specific administration of a compound, such as at the site of a tumor. *Ex vivo* refers to performing part of the regulatory step outside of the patient, such as by transfecting a population of cells removed from a patient with a recombinant molecule comprising a nucleic acid sequence encoding a protein according to the present invention under conditions such that the recombinant molecule is subsequently expressed by the transfected cell, and returning the transfected cells to the patient. *In vitro* and *ex vivo* routes of administration of a composition to a culture of host cells can be accomplished by a method including, but not limited to, transfection, transformation, electroporation, microinjection, lipofection, adsorption, protoplast fusion, use of protein carrying agents, use of ion carrying agents, use of detergents for cell permeabilization, and simply mixing (e.g., combining) a compound in culture with a target cell.

In the method of the present invention, a therapeutic compound, including agonists and antagonists of progesterone receptors, as well as compositions comprising such compounds, can be administered to any organism, and particularly, to any member of the Vertebrate class, Mammalia, including, without limitation, primates, rodents, livestock and domestic pets. Livestock include mammals to be consumed or that produce useful products (e.g., sheep for wool production). Preferred mammals to protect include humans. Typically, it is desirable to modulate (e.g., regulate (up or down)) progesterone receptor biological activity or the biological activity of a gene regulated by a PR, to obtain a therapeutic benefit in a patient. A therapeutic benefit is not necessarily a cure for a particular disease or condition, but rather, preferably encompasses a result which can include alleviation of the disease or condition, elimination of the disease or condition, reduction of a symptom associated with the disease or condition, prevention or alleviation of a secondary disease or

condition resulting from the occurrence of a primary disease or condition, and/or prevention of the disease or condition. As used herein, the phrase "protected from a disease" refers to reducing the symptoms of the disease; reducing the occurrence of the disease, and/or reducing the severity of the disease. Protecting a patient can refer to the ability of a composition of the present invention, when administered to a patient, to prevent a disease from occurring and/or to cure or to alleviate disease symptoms, signs or causes. As such, to protect a patient from a disease includes both preventing disease occurrence (prophylactic treatment) and treating a patient that has a disease (therapeutic treatment) to reduce the symptoms of the disease. A beneficial effect can easily be assessed by one of ordinary skill in the art and/or by a trained clinician who is treating the patient. The term, "disease" refers to any deviation from the normal health of a mammal and includes a state when disease symptoms are present, as well as conditions in which a deviation (e.g., infection, gene mutation, genetic defect, etc.) has occurred, but symptoms are not yet manifested.

The following examples are provided for the purpose of illustration and are not intended to limit the scope of the present invention.

EXAMPLES

Example 1

The following example describes the identification of genes regulated by progesterone receptors.

Materials and Methods

Cell Culture

Wild-type PR-positive T47Dco breast cancer cell line and its clonal derivatives T47D-Y, T47D-YA and T47D-YB, have been described (Horwitz et al., *Cell* 28, 633-42 (1982); Sartorius *et al.*, *Cancer Res.* 54, 3668-3877 (1994)). Briefly, cells are routinely cultured in 75 cm^2 plastic flasks and incubated in 5% CO_2 at 37°C in a humidified environment. The stock medium consists of Eagle's Minimum Essential Medium with Earle's salts (MEM), containing L-glutamine (292 mg/liter) buffered with sodium

bicarbonate (2.2 g/liter), insulin (6ng/ml) and 5% fetal bovine serum (Hyclone, Logan, UT) with G418.

Arrays

Atlas™ Human cDNA Expression Array. T47D-YA and T47D-YB breast cancer cells were grown to mid-confluence in Minimal Essential Medium containing 5% Fetal Calf Serum, then either treated with 10 nM progesterone dissolved in ethanol for 6 or 12 hours, or in ethanol alone. This yielded 4 treatment types. Total RNA was prepared from the 4 sets of cells using guanidinium isothiocyanate, polyA$^+$ RNA was purified with the Oligotex mRNA Kit (Qiagen, Valencia, CA), and ^{32}P-labeled cDNA was synthesized from 1ug of each sample using SuperScriptII reverse transcriptase (Gibco BRL Life Technologies, Gaithersburg, MD). Labeled probes were separately hybridized to Atlas™ Human cDNA Expression Arrays (Clontech, Palo Alto, CA) consisting of nylon membranes onto which 588 cDNA fragments encoding known proteins were spotted in duplicate. After a high stringency wash, hybridization was detected by autoradiography and phosphoimaging on a Molecular DynamicsPhosphoImager™ (Molecular Dynamics, Sunnyvale, CA). Data were analyzed using Atlas™ Image 1.0, and normalized to signals from control housekeeping genes on the same filter. For selected genes, progesterone inducibility and PR-isoform specificity were confirmed by northern blotting, reverse transcriptase-polymerase chain reaction (RT-PCR), and/or western blotting.

Affymetrix GeneChip™ Array. T47D-Y, T47D-YA and T47D-YB breast cancer cells were grown to mid-confluence in Minimal Essential Medium containing 5% Fetal Calf Serum, then either treated with 10 nM progesterone dissolved in ethanol for 6 hours, or in ethanol alone. This yielded 6 treatment types. Total RNA and polyA$^+$ RNA were prepared from the 6 sets, as described above. First strand cDNA was synthesized from 2ug of polyA$^+$ RNA using SSII Reverse Transcriptase, the T7dT 24mer, and other components of the Superscript Choice system (Gibco BRL Life Technologies, Gaithersburg, MD). Following second strand synthesis, the DNA was purified by phenol/chloroform extraction and precipitation, and resuspended in 12ul DEPC-treated RNase water. 5ul were used in an *in vitro* transcription reaction using the EnZo BioArray™ High Yield transcript Labeling Kit (Affymetrix, Inc., Santa Clara, CA), to synthesize RNA transcripts and incorporate biotin

labeled ribonucleotides. Unincorporated nucleotides were removed with RNeasy affinity columns (Qiagen, Valencia, CA). Purified, biotinylated cRNAs were quantified, and 20ug were subjected to a fragmentation reaction by incubation at 94C for 35 min (Affymetrix™ protocol 700218) to randomly generate fragments ranging from 35 to 200 bases. HuGeneFL Array™ chips consisting of 5,600 full-length human genes from Unigene, Genebank and TIGR databases were used for hybridization. Thirty µl of fragmented cRNA were added to a hybridization mixture (100mM MES, 1M NaCl, 20mMEDTA, and 0.01% Tween 20) and control oligonucleotide B2 and control cRNA cocktail, as described in the Affymetrix™ protocol. Hybridizations and subsequent washes were done in the GeneChip Hybridization Oven and Fluidics Station 400. After overnight hybridization, the solutions were removed, the chips were washed and stained with streptavidin-phycoerythrin. DNA chips were read at a resolution of 6um with a Hewlett-Packard GeneArray Scanner.

Each gene on the chip is represented by perfectly matched (PM) and mismatched (MM) oligonucleotides from 16-20 regions of each gene. The mismatched probes act as specificity controls, which allow direct subtraction of background and cross-hybridization signals. The number of instances in which the PM hybridization signal is larger that the MM signal is computed along with the average of the logarithm of the PM:MM ratio (after background subtraction) for each probe set. These values were used to arrive at a matrix-based decision concerning the presence or absence of an RNA transcript. Detailed protocols for data analyses of Affymetrix microarrays and extensive documentation of the sensitivity and quantitative aspects of the method have been described. Briefly, the first level of analysis including the "present" or "absent" call, and pairwise comparisons, were done using GeneChip 3.1 Expression Analysis Program ™ (Affymetrix, Inc., Santa Clara, CA). A second level of analysis to identify clusters of genes regulated by progesterone via PR-A, PR-B or both was performed using GeneSpring™ version 3.0 (Silicon Genetics, San Carlos, CA). The present inventors used customized software capable of comparing multiple experimental pairwise comparisons (minus versus plus progesterone) and multiple control comparisons (all minus hormone samples and all plus hormone samples) to compare fold change minus versus plus hormone as compared to the fold change between controls. This served as a measure of the variability between samples. As a third level of analysis, k-means

clustering was performed using GeneSpring™ version 3.2.12 (Silicon Genetics, San Carlos, CA) to identify patterns of gene regulation in PR-A, PR-B, or PR-negative cells treated with or without progesterone.

Selected genes, *i.e.,* ones that were substantially regulated or are of particular biological interest, have been confirmed by northern and/or RT-PCR, and/or by western blotting. Additionally, the promoters of several genes of interest have been cloned, linked upstream of a luciferase reporter, and tested for their ability to be transcriptionally regulated by PR-A *vs.* PR-B after transfection into HeLa cervicocarcinoma cells, followed by progesterone treatment of the cells. In the examples tested, regulation by PR-A vs. PR-B using the synthetic promoter/reporter constructs, mimicked the regulation of the endogenous genes in the breast cancer cells, supporting the use of these approaches for drug discovery.

RT-PCR and Northern Blot Analysis

RT-PCR amplifications of target sequences were performed with co-amplification of an internal control sequence (β2MG or GAPDH) using:

β2MG forward primer: 5'-ATCCAGCGTACTCCAAAGATTC-3' (SEQ ID NO:1);

β2MG reverse primer: 5'-TCCTTGCTGAAAGACAAGTCTG-3' (SEQ ID NO:2);

resulting in a product of 178 bp. GAPDH primers yielded a product of 485 bp. GAPDH, Integrin α6, and bcl-x cDNA primer sequences were obtained from Clontech. Total RNA was prepared from T47DY-A or -B cells as described above. One μg of RNA was mixed with 0.4 μM random hexamers and heated to 65°C for five min. (Perkin Elmer). 1X PCR buffer (5 mM $MgCl_2$), 20 U RNAse inhibitor, 4 mM dNTPs, and 125 U MMLV reverse transcriptase were added and tubes were incubated at 42°C for 1 hour. Five μl of the cDNA synthesis reactions were added to 1X PCR buffer, 1.8 mM $MgCl_2$, 10mM dNTP blend, and 60 pmoles of specific primers were incubated with 5 U AmpliTaq DNA polymerase at 94°C for 30 s, 65 C for 45 s, and 68°C for 1 min for 16-18 cycles (cycle number was chosen to be in the linear range of amplification for each product). All PCR reagents were purchased from Perkin Elmer, Foster City, CA. Five μl of samples were resolved on a 2% agarose gel, and Southern blots were performed in 0.4M. Blots were prehybridized in Rapid-hyb (Amersham) for 1h at 65°C. cDNA probes were generated by RT-PCR and radioactively labeled using MegaPrime DNA labeling system (Amersham) and ^{32}P-αdCTP. Blots were

probed for 2 h to overnight at 65°C. Blots were washed and exposed to autoradiography film or phosphoimaging screen and then quantified using ImageQuant, Molecular Dynamics. In some cases the RT-PCR products could be visualized on an ethidium bromide stained gel when amplified in the linear range of production and in these cases Southern blotting and hybridizing with a labeled probe was unnecessary and products were instead directly quantitated. In some cases Northern blot analysis was used to detect transcripts. In these cases 25 μg of total RNA was electrophoresed in a formaldehyde agarose gel and transferred to a Hybond nylon membrane (Amersham) and hybridized sequentially with cDNA inserts for specific genes generated by random priming PCR products generate as above with ^{32}P-dCTP using Mega-Prime DNA Labeling Kit (Amersham). Membranes were then probed with fragments of housekeeping genes (either B2MG or GAPDH).

Transcriptional assay:

HeLa cells plated at 4 x 10^5 cells per 10cm dish in MEM supplemented with 5% fetal bovine serum were then transiently transfected with 100ng of HPR1 (PR-B in pSG5) or HPR2 (PR-A in pSG5) and 1.2 μg of the integrin α6 promoter (-740) in pGL3-Basic vector plasmid (gift from Dr. Sohei Kitazawa, Kobe University School of Medicine , Department of Pathology), 1.2 μg of β-galactosidase expression plasmid pCH110, and 5.5 μg BSM. treated with 10 nM progesterone or ethanol vehicle for 24 hours.

Immunoblots:

For time course treatments with progesterone, cells were plated at 2 million cells per large plates in MEM with supplements described above and were treated with 10 nM progesterone (Sigma). Cells were harvested in RIPA buffer (10 mM sodium phosphate, pH 7.0, 150 mM NaCl, 2mM EDTA, 1% deoxycholic acid, 1% Nonedet P-40, 0.1% SDS, 0.1% β-mercaptoethanol, 1 mM PMSF, 50 mM sodium fluoride, 200 μM Va_3VO_4, and one Complete Protease Inhibitor Mixture tablet (Boehringer Mannheim, GmbH Germany) per 50 mls of RIPA buffer made fresh for each use. Protein extracts were equalized to 150 μg by Bradford assay (Bio-Rad), resolved by SDS-PAGE, and transferred to nitrocellulose. Equivalent protein loading was confirmed by Ponceau S staining. Following incubation with the appropriate antibodies, and HRP-conjugated secondary antibodies, protein bands were detected by enhanced chemiluminescence (Amersham, Arlington Heights, IL).

Results

Gene expression data from Affymetrix HuGeneFL Array™ chips were analyzed using Microarray Suite 4.0 Expression Analysis Program (Affymetrix™). Experimental data from independent triplicate experiments for T47D-YA and T47D-YB cells and duplicate T47D-Y cells treated with or without 10nM progesterone were analyzed and pairwise comparisons were performed to identify genes that had increased or decreased with addition of hormone. These data were imported into Microsoft Excel and custom formulas were written to identify genes that had repeatedly increased or decreased with hormone in three out of three experiments by at least 1.8 fold, but did not vary more than two fold between control groups. Genes that met these criteria and were up- or downregulated by progesterone by in PR-B containing cells are shown in Table 18, while those up- or downregulated by progesterone in PR-A containing cells are shown in Table 19. In both tables fold increases and decreases (negative numbers) upon treatment with progesterone for 6 hrs are indicated. Genes which were at below detectable levels and called absent in one sample, but which were detectable and called as present in the other are denoted with a tilde beside the fold changes. The fold changes indicated with a tilde cannot be compared to those that are not marked with a tilde (indicating they were present in both minus and plus hormone samples) as the fold change was calculated by setting the undetectable gene to background level. Genes in bold in Table 18 are uniquely regulated by progesterone only via PR-B, while those in bold in Table 19 are uniquely regulated by PR-A; those not bolded were regulated in both PR-B and PR-A containing cells. Only genes that were regulated in 3 out of 3 experiments are shown and average fold inductions are given. Genes marked with an asterisk were identified from Atlas™ Human cDNA Expression Arrays (Clonetech, Palo Alto, CA) and those marked by an & symbol were identified as being progesterone regulated on using both Atlas™ Human cDNA Expression Arrays and Affymetrix HuGeneFL Array™ chips (Affymetrix, Inc., Santa Clara, CA), all others were identified using Affymetrix HuGeneFL Array™ chips (Affymetrix, Inc., Santa Clara, CA). The present inventors have categorized genes regulated by progesterone in this study into functional categories based on GeneCard information as well as extensive literature reviews of each gene product (Table 17). Ten of the genes found to be regulated by progesterone in the present study have previously been

reported by other groups to be progesterone responsive in either breast cancer cells or other hormone responsive cell types or tissues (Table 8). However, the PR-A and/or PR-B isoform specificity of these genes was unknown prior to the present invention. The independent identification of genes that have previously been reported to be progesterone-regulated serves as an internal control and also demonstrates the sensitivity of this assay, as even genes induced by progesterone as little as 1.9 fold were detected on the arrays. Additionally, 8 of the genes found to be regulated by progesterone in the present study have previously been reported to be involved in either breast cancer or mammary gland development (Table 16).

The average differences indicating relative intensities obtained from triplicate experiments from T47D-YA and T47D-YB cell lines and duplicate experiments in the PR-negative T47D-Y cells were entered into GeneSpring™ 3.2.12 (Silicon Genetics, San Carlos, CA). To normalize for variation among chips each gene intensity value was normalized to 1 (intensity of gene A on chip X divided by the median of all intensities measured on chip X). To identify patterns of gene expression among cell lines and hormone treatments, k-means clustering was performed. Clustergrams of various patterns of gene regulation were generated. Within these clusters, any one gene can be viewed individually and standard error bars generated from replicate experiments are shown for gene expression levels in cell lines containing either PR-A, PR-B, or no PR, with or without progesterone treatment. A cluster of genes was shown to be upregulated by progesterone in both PR-A and PR-B containing cells, but not in the PR-negative cell line. While most of these genes were upregulated by progesterone treatment more strongly via PR-B, some, such as S100P calcium binding protein, and Grb10 are upregulated equally well via PR-A and PR-B. Upregulation of IkappaBalpha via both receptors was confirmed at the protein level as early as 6 hours, and remained elevated for up to 48 hours in the presence of progesterone (data not shown). Additionally, the gene encoding Ezrin, identified as being progesterone regulated using Atlas™ Human cDNA Expression Arrays probed with RNA from T47D-YA and YB cells left untreated or treated with progesterone for 12 hrs was confirmed to be equally well upregulated by both PR-A and PR-B at 12, 24 and 48 hrs by northern blot analysis (data not shown).

The present inventors have demonstrated that although some genes (and their protein products) are regulated by progesterone through both PR isoforms, many genes are uniquely regulated by either PR-A or PR-B. In the T47D breast cancer cell lines used for the present invention, many more genes were regulated by progesterone through PR-B than through PR-A. However, it remains to be determined whether this situation is reversed in other types of cells or tissues; the endometrium for instance. Data from knock-out mice show that PR-A, but not PR-B, plays an important role in opposing the proliferative effect of estrogen on the endometrium. This is one example of tissue and PR isoform specificity (Mulac-Jericevic et al., *Science* **289**, 1751-4 (2000)).

Many progesterone regulated genes require PR-B as illustrated by Tables 3, 4, 11, 12 and 18. Two examples are Stat5a and C/EBP beta. Their differential upregulation only by PR-B was confirmed by immunoblot at several time-points after progesterone treatment (data not shown). In contrast, the same western blot probed for two control proteins, p21 and cyclin D1, previously reported to be progesterone regulated (Musgrove *et al.*, *Mol. Cell. Biol.* **13**, 3577-3587 (1993); Musgrove et al., *Mol. Endocrinol.* **11**, 54-66 (1997); Groshong *et al.*, *Mol Endocrinol* **11**, 1593-607 (1997)), showed them to be equally well regulated by either PR-A or PR-B. The gene encoding tissue factor is also uniquely regulated by PR-B. This too was confirmed by RT-PCR. Similarly, RT-PCR confirmed that integrin alpha 6 is uniquely regulated by PR-B at 6, 12, and 24 hours after progesterone treatment. To demonstrate the differential regulation of this gene by PR-B in a different cell line and by different methods, the present inventors transfected the integrin alpha 6 promoter linked to luciferase into progesterone treated PR-negative HeLa cells that were cotransfected with either PR-B or PR-A. Transcription of the integrin alpha 6 promoter was induced 4.4 fold by PR-B, but was not regulated at all by PR-A, or by cells lacking PR (not shown).

Fewer genes were uniquely regulated by PR-A (Table 19) and they tended to be expressed at relatively low levels. The gene encoding the docking protein enhancer of filamentation was significantly upregulated only by PR-A. The gene encoding the estrogen related receptor (ERR), which can heterodimerize with ERα and Erβ is also PR-A dependent. The preferential upregulation of ERR by PR-A was confirmed by RT-PCR at both 6 and 12

hrs of progesterone treatment. The anti-apoptosis inducing protein Bcl-X_L, is another gene uniquely regulated by PR-A as confirmed by RT-PCR (not shown).

In general, fewer genes were downregulated by progesterone treatment than were upregulated (Tables 18 and 19). Analysis of pairwise comparisons using MicroArray Suite 4.0 Expression Analysis Program™ was used to demonstrate the statistical significance of the downregulation (in 3 out of 3 experiments). Similarly, gene filtering using GeneSpring™ generated a clustergram of downregulated genes (data not shown) confirming the accuracy of the assignments. Of the downregulated genes, three were downregulated by both PR-A and PR-B; eleven were uniquely downregulated by PR-B; and two were uniquely downregulated by PR-A. Downregulation of three of these genes, monocyte chemotactic protein, bullous pemphigoid antigen, and transforming growth factor-beta 3 (TGF-beta 3) was confirmed by RT-PCR (data not shown).

Several genes that were identified by the present inventors as being regulated by progesterone, were previously known to be important in breast cancers. Based on the present invention they may now be targeted for specific progestin therapies. (1) For instance, S100P calcium-binding protein overexpression is associated with immortalization of human breast epithelial cells *in vitro* and with early stages of breast cancer development *in vivo* (Guerreiro da Silva *et al.*, *Int J Oncol* **16**, 231-40 (2000)). (2) The gene encoding tissue factor, a cell surface glycoprotein, is associated with metastasis in breast and other types of cancers (Ueno *et al.*, *Br J Cancer* **83**, 164-70 (2000); Lwaleed et al., *J Pathol* **187**(3):291-4 (1999)). Tissue factor was previously known to be regulated by progesterone in the endometrium (Krikun *et al.*, *Mol Endocrinol* **14**, 393-400 (2000); Lockwood *et al.*, *J Clin Endocrinol Metab* **85**, 297-301 (2000); Krikun *et al.*, *J Clin Endocrinol Metab* **83**, 926-30 (1998)), but not in the breast or in breast cancers. (3) The gene encoding Gas6, a ligand for the tyrosine kinase receptor Axl receptor tyrosine kinase (RTK) and other members of the RTK family, was recently reported to be mitogenic in breast cancer cells (Goruppi et al., *Mol Cell Biol* **21**, 902-915 (2001)) and it promotes angiogenesis (Fridell et al., *J Biol Chem* **273**, 7123-6. (1998)). (4) The HEF1 gene is highly related to BCAR1/p130Cas, which has been found to be upregulated in tamoxifen resistant tumors (van der Flier et al., *Int J Cancer* **89**, 465-8 (2000); van der Flier *et al.*, *J Natl Cancer Inst* **92**, 120-7 (2000)). The present invention

provides the rationale for measuring the expression levels of these genes in breast cancers. It may be that tumors that overexpress these genes good candidates for suppressive therapy with progesterone antagonists.

Additionally the inventors now demonstrate the progesterone regulation of several genes previously known to be preferentially expressed in normal breast epithelium compared to breast cancers. For instance, the gene encoding bullous pemphigoid antigen, a protein associated with hemidesmosomes, is overexpressed 12-fold in normal breast cells compared to breast tumors (Nacht *et al.*, *Cancer Res* **59**, 5464-70 (1999)). Such desmosomes are important in maintaining the normal differentiated architecture of the breast. The present inventors have found that bullous pemphigoid antigen is downregulated by progesterone through both PR isoforms. This down regulation may be harmful, and/or it may disrupt important cell-cell interactions. It is possible that antiprogestin therapy would prevent this downregulation.

Some of the genes that were discovered by the present inventors to be progesterone regulated are involved in particular functional pathways. Groups of temporally regulated genes are often involved in the same pathway. For example, it was previously known that progesterone regulates genes involved in the steroid biosynthesis and trafficking pathways (Watari *et al.*, *Exp Cell Res* **259**, 247-56 (2000); Darnel et al., *J Steroid Biochem Mol Biol* **70**:203-10 (1999); Arcuri et al., *Endocrinology* **137**:595-600 (1996)), and the present investigators identify a cluster of such genes. However, less is known about the role of progesterone in regulating signaling pathways controlled by growth factors and cytokines. The present inventors' data demonstrate for the first time, that progesterone plays an important role in regulating many genes involved in these signaling pathways. In addition, the present inventors' demonstrate that progesterone regulates expression of genes for proteins previously known to interact with PR. Examples are FKB54 (Kester et al., *J Biol Chem* **272**, 16637-43 (1997)), Stat5 (Richer *et al.*, *J Biol Chem* **273**, 31317-26 (1998)), IκBα and cytoplasmic dynein light chain 1 (Crepieux *et al.*, *Mol Cell Biol* **17**:7375-85 (1997)).

Table 1. Genes selectively upregulated by PR-A

Accession No.	Fold Increase	Gene Name
L43821	4.7	enhancer of filamentation (HEF1)
L38487	2.3	estrogen receptor-related protein (hERRa1)

Table 2. Genes selectively downregulated by PR-A

Accession No.	Fold Decrease	Gene Name
U44103	-2.8	small GTP binding protein Rab9

Table 3. Genes selectively upregulated by PR-B.

Accession No.	Fold Increase	Gene Name
L13720	~23.1	growth arrest-specific protein (gas6)
M27436	~18.1	tissue factor gene
D79990	10.2	KIAA0168 Ras association (RalGDS/AF-6) domain family 2 (RASSF2)
U01120	~9.8	glucose-6-phosphatase
D25539	~8	KIAA0040 gene
U37546	~7.2	IAP homolog C (MIHC)
D87953	6.8	RTP,DRG1,CAP43
M76180	~6.5	aromatic amino acid decarboxylase (ddc)
M77140	~6	pro-galanin
D50840	~5.6	ceramide glucosyltransferase
HG2743-HT2846	~5.1	Caldesmon 1 Non-Muscle
U76421	~4.7	dsRNA adenosine deaminase DRADA2b
U40572	4.6	beta2-syntrophin (SNT B2)
S69189	~4.5	peroxisomal acyl-coenzyme A oxidase
U44754	4.4	PSE-binding factor PTF gamma subunit
U02081	4.1	guanine nucleotide regulatory protein (NET1) oncogene[1]
D16227	~4	BDP-1 (member of the recoverin family)
D17793	~4	3-alpha hydroxysteroid dehydrogenase type IIb
U83461	3.7	putative copper uptake protein (hCTR2)
M23254	3.6	Ca2+-activated neutral protease (CANP)
D15050	3.6	transcription factor AREB6
HG2167-HT2237	~3.5	Protein Kinase Ht31, Camp-Dependent
D10040	3.5	long-chain acyl-CoA synthetase
D31887	3.5	KIAA0062 gene
X60673	3.4	adenylate kinase 3
U45878	~3.3	inhibitor of apoptosis protein 1
L09229	3.3	long-chain acyl-coenzyme A synthetase (FACL1)
U09646	3.2	carnitine palmitoyltransferase II precursor (CPT1)
D31716	3.2	GC box bindig protein
M37400	3.1	cytosolic aspartate aminotransferase
X59834	3.1	glutamine synthase
D78335	3.1	uridine monophosphate kinase (UMPK)
U41387	3	RNA helicase II/Gu)
U07919	3	aldehyde dehydrogenase 6
M69013	2.9	guanine nucleotide-binding regulatory protein (G-y-alpha)[1]
HG2530-HT2626	2.9	Adenylyl Cyclase-Associated Protein 2
U79288	2.8	clone 23682
D10704	2.6	choline kinase
Y08134	2.6	ASM-like phosphodiesterase 3b
U33632	2.6	two P-domain K+ channel TWIK-1
M21154	2.5	S-adenosylmethionine decarboxylase
U77949	2.5	Cdc6-related protein (HsCDC6)
M95767	~2.5	di-N-acetylchitobiase
D83781	2.5	KIAA0197 gene
X98534	2.5	vasodilator-stimulated phosphoprotein (VASP)
X53586	2.5	Integrin α 6*
D80001	2.4	KIAA0179 gene
L18960	2.4	protein synthesis factor (eIF-4C)

Table 3. cont'd..

D23673	2.3	insulin receptor substrate-1 (IRS-1)
J02888	2.3	quinone oxidoreductase (NQO2)
D63487	2.3	KIAA0153 gene
U14603	2.3	protein-tyrosine phosphatase (HU-PP-1)
L41887	2.3	splicing factor, arginine/serine-rich 7 (SFRS7)
M92287	2.2	cyclin D3 (CCND3)
X61123	2.2	BTG1
M95929	2.1	homeobox protein (PHOX1)
U32944	2.1	cytoplasmic dynein light chain 1 (hdlc1)
D79994	2.1	KIAA0172 gene (similar to ankyrin)
D89377	2	MSX-2
U90878	2	LIM domain protein CLP-36
U97105	2	N2A3 dihydropyrimidinase related protein-2
L40379	2	thyroid receptor interactor (TRIP10)
J05459	1.9	glutathione transferase M3 (GSTM3)
L42542	1.8	RLIP76 (ralA binding protein 1)
D42047	1.7	KIAA0089 similar to glycerol-3-phosphate dehydrogenase 1
M84349	1.7	transmembrane protein (CD59)
D43950	1.6	KIAA0098 T-COMPLEX PROTEIN 1 (TCP-1-EPSILON)
M15796	1.6	proliferating cell nuclear antigen (PCNA)

Table 4. Genes selectively downregulated by PR-B

Accession No.	Fold Decrease	Gene Name
U07225	~-4.3	P2U nucleotide receptor
M27492	~-3.4	interleukin 1 receptor mRNA
Y08682	-3.1	carnitine palmitoyltransferase I type I
U29091	~-2.9	selenium-binding protein (hSBP)
X79683	-2.6	beta2 laminin.
AB000220	-2.6	semaphorin E[1]
HG2197-HT2267	~-2.5	Collagen, Type Vii, Alpha 1
U65011	~-2.5	preferentially expressed antigen of melanoma (PRAME)
M18391	~-2.3	tyrosine kinase receptor (eph)
X71874	-1.9	proteasome-like subunit MECL-1

Table 5. Genes up or downregulated by both PR-A and PR-B

Accession No.	Fold	Gene Name
X51521	~22.6	Ezrin*
U70663	~7.5	zinc finger transcription factor EZF
U16799	6.1	Na,K-ATPase beta-1 subunit
X65614	3.6	calcium-binding protein S100P
D86962	2.9	Grb10
S81914	2.6	IEX-1=radiation-inducible immediate-early
U00115	2.4	bcl-6
M69225	~-3.5	bullous pemphigoid antigen (plakin family)
U90907	-3.2	clone 23907
M92357	-2.1	tumor necrosis factor alpha-induced protein 2 (B94)

Table 6. Gene that is reciprocally regulated (upregulated by PR-B, downregulated by PR-A)

Accession No.	Fold	Gene Name
X53586	2.5	Integrin α 6*

Table 7. Group of genes for which the expression level is different depending on which isoform is present.

Accession No.	Fold	Gene Name
L13720	~23.1	growth arrest-specific protein (gas6)
D79990	10.2	KIAA0168 Ras association (RalGDS/AF-6) domain family 2 (RASSF2)
U01120	~9.8	glucose-6-phosphatase
U37546	~7.2	IAP homolog C (MIHC)
D87953	6.8	RTP,DRG1,CAP43
M76180	~6.5	aromatic amino acid decarboxylase (ddc)
M77140	~6	pro-galanin
D50840	~5.6	ceramide glucosyltransferase
HG2743-HT2846	~5.1	Caldesmon 1 Non-Muscle
U76421	~4.7	dsRNA adenosine deaminase DRADA2b
U40572	4.6	beta2-syntrophin (SNT B2)
S69189	~4.5	peroxisomal acyl-coenzyme A oxidase
U44754	4.4	PSE-binding factor PTF gamma subunit
U02081	4.1	guanine nucleotide regulatory protein (NET1) oncogene
D16227	~4	BDP-1 (member of the recoverin family)
D17793	~4	3-alpha hydroxysteroid dehydrogenase type IIb
U83461	3.7	putative copper uptake protein (hCTR2)
M23254	3.6	Ca2+-activated neutral protease (CANP)
D15050	3.6	transcription factor AREB6
HG2167-HT2237	~3.5	Protein Kinase Ht31, Camp-Dependent
D10040	3.5	long-chain acyl-CoA synthetase
D31887	3.5	KIAA0062 gene
X60673	3.4	adenylate kinase 3
U45878	~3.3	inhibitor of apoptosis protein 1
L09229	3.3	long-chain acyl-coenzyme A synthetase (FACL1)
U09646	3.2	carnitine palmitoyltransferase II precursor (CPT1)
D31716	3.2	GC box bindig protein
M37400	3.1	cytosolic aspartate aminotransferase
X59834	3.1	glutamine synthase
D78335	3.1	uridine monophosphate kinase (UMPK)
U41387	3	RNA helicase II/Gu)
U07919	3	aldehyde dehydrogenase 6
M69013	2.9	guanine nucleotide-binding regulatory protein (G-y-alpha)
HG2530-HT2626	2.9	Adenylyl Cyclase-Associated Protein 2
U79288	2.8	clone 23682
D10704	2.6	choline kinase
Y08134	2.6	ASM-like phosphodiesterase 3b
U33632	2.6	two P-domain K+ channel TWIK-1
M21154	2.5	S-adenosylmethionine decarboxylase
U77949	2.5	Cdc6-related protein (HsCDC6)
M95767	~2.5	di-N-acetylchitobiase
D83781	2.5	KIAA0197 gene
X98534	2.5	vasodilator-stimulated phosphoprotein (VASP)
D80001	2.4	KIAA0179 gene
L18960	2.4	protein synthesis factor (eIF-4C)
D23673	2.3	insulin receptor substrate-1 (IRS-1)
J02888	2.3	quinone oxidoreductase (NQO2)
D63487	2.3	KIAA0153 gene

Table 7. cont'd....

U14603	2.3	protein-tyrosine phosphatase (HU-PP-1)
L41887	2.3	splicing factor, arginine/serine-rich 7 (SFRS7)
M92287	2.2	cyclin D3 (CCND3)
X61123	2.2	BTG1
M95929	2.1	homeobox protein (PHOX1)
U32944	2.1	cytoplasmic dynein light chain 1 (hdlc1)
D79994	2.1	KIAA0172 gene (similar to ankyrin)
D89377	2	MSX-2
U90878	2	LIM domain protein CLP-36
U97105	2	N2A3 dihydropyrimidinase related protein-2
L40379	2	thyroid receptor interactor (TRIP10)
J05459	1.9	glutathione transferase M3 (GSTM3)
L42542	1.8	RLIP76 (ralA binding protein 1)
D42047	1.7	KIAA0089 similar to glycerol-3-phosphate dehydrogenase 1
M84349	1.7	transmembrane protein (CD59)
D43950	1.6	KIAA0098 T-COMPLEX PROTEIN 1 (TCP-1-EPSILON)
M15796	1.6	proliferating cell nuclear antigen (PCNA)
U07225	~-4.3	P2U nucleotide receptor
M27492	~-3.4	interleukin 1 receptor mRNA
Y08682	-3.1	carnitine palmitoyltransferase I type I
U29091	~-2.9	selenium-binding protein (hSBP)
X79683	-2.6	beta2 laminin.
AB000220	-2.6	semaphorin E
HG2197-HT2267	~-2.5	Collagen, Type Vii, Alpha 1
U65011	~-2.5	preferentially expressed antigen of melanoma (PRAME)
M18391	~-2.3	tyrosine kinase receptor (eph)
X71874	-1.9	proteasome-like subunit MECL-1
L43821	4.7	enhancer of filamentation (HEF1)
L38487	2.3	estrogen receptor-related protein (hERRa1)
D25539	~8	KIAA0040 gene

Table 8. Genes encoding products previously reported to be regulated by progesterone

Accession no.	Gene Name	Cell or tissue type	Isoform
U26726	11-beta-hydroxysteroid dehydrogenase type 2	endometrial stromal cells, endometrial cancer cells,	Both[1]
M27436	tissue factor gene	endometrium	PR-B only[2]
U42031	progesterone receptor-associated FKBP54	breast cancer cells	Both[3]
M68516	PCI gene (plasminogen activator inhibitor)	endometrial stromal cells	PR-B only[4]
U43185	Stat5A	breast cancer cells	PR-B only[5]
X52730	phenylethanolamine n-methyltransferase (PNMT)	adrenal medulla	PR-B only[6]
M69043	MAD-3 encoding IkB-alpha	macrophage cells and endometrium	Both[7]
AF002020	Niemann-Pick C disease (NPC1)	granulosa cells	PR-B only[8]
D00017	lipocortin II (calpactin I)	endometrial cancer cells	PR-B only[9]
D25328	platelet-type phosphofructokinase	breast cancer cells, intestinal epithelium, granulosa cells	PR-B only[10]
M80254	cyclophilin isoform (hCyP3)	liver	PR-B only[11]
HG4069-HT4339_s_at	Monocyte Chemotactic Protein 1	endometrial cells and breast cancer cells	PR-A only[12]
Z50781	delta sleep inducing peptide (related to TSC-22)	breast cancer cells	PR-A only[13]

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Table 9. Genes selectively upregulated by PR-A

Accession No.	Fold Increase	Gene Name
L43821	4.7	enhancer of filamentation (HEF1)
Z23115	3.2	Bcl-x*
Z50781	2.5	delta sleep inducing peptide (higly related to TSC-22)
L38487	2.3	estrogen receptor-related protein (hERRa1)

Table 10. Genes selectively downregulated by PR-A

Accession No.	Fold Decrease	Gene Name
HG4069-HT4339	-7.4	Monocyte Chemotactic Protein 1
U44103	-2.8	small GTP binding protein Rab9

Table 11. Genes selectively upregulated by PR-B

Accession No.	Fold Increase	Gene Name
L13720	~23.1	growth arrest-specific protein (gas6)
M27436	~18.1	tissue factor gene
D79990	10.2	KIAA0168 Ras association (RalGDS/AF-6) domain family 2 (RASSF2)
U01120	~9.8	glucose-6-phosphatase
D25539	~8	KIAA0040 gene
U37546	~7.2	IAP homolog C (MIHC)
D87953	6.8	RTP,DRG1,CAP43
M76180	~6.5	aromatic amino acid decarboxylase (ddc)
M83667	6.4	NF-IL6 (C/EBPbeta)
M68516	~6.2	PCI gene (plasminogen activator inhibitor 3)
U43185	~6.1	Stat5A
M77140	~6	pro-galanin
D50840	~5.6	ceramide glucosyltransferase
HG2743-HT2846	~5.1	Caldesmon 1 Non-Muscle
U76421	~4.7	dsRNA adenosine deaminase DRADA2b
U40572	4.6	beta2-syntrophin (SNT B2)
S69189	~4.5	peroxisomal acyl-coenzyme A oxidase
U44754	4.4	PSE-binding factor PTF gamma subunit
X52730	4.4	phenylethanolamine n-methyltransferase (PNMT)
U02081	4.1	guanine nucleotide regulatory protein (NET1) oncogene[1]
D16227	~4	BDP-1 (member of the recoverin family)
D17793	~4	3-alpha hydroxysteroid dehydrogenase type IIb
U83461	3.7	putative copper uptake protein (hCTR2)
M23254	3.6	Ca2+-activated neutral protease (CANP)
D15050	3.6	transcription factor AREB6
HG2167-HT2237	~3.5	Protein Kinase Ht31, Camp-Dependent
D10040	3.5	long-chain acyl-CoA synthetase
D31887	3.5	KIAA0062 gene
X60673	3.4	adenylate kinase 3
U45878	~3.3	inhibitor of apoptosis protein 1
L09229	3.3	long-chain acyl-coenzyme A synthetase (FACL1)
U09646	3.2	carnitine palmitoyltransferase II precursor (CPT1)
D31716	3.2	GC box bindig protein
M37400	3.1	cytosolic aspartate aminotransferase
X59834	3.1	glutamine synthase
D78335	3.1	uridine monophosphate kinase (UMPK)
U41387	3	RNA helicase II/Gu)
U07919	3	aldehyde dehydrogenase 6
M69013	2.9	guanine nucleotide-binding regulatory protein (G-y-alpha)[1]
HG2530-HT2626	2.9	Adenylyl Cyclase-Associated Protein 2
U79288	2.8	clone 23682
D10704	2.6	choline kinase
Y08134	2.6	ASM-like phosphodiesterase 3b
U33632	2.6	two P-domain K+ channel TWIK-1
M21154	2.5	S-adenosylmethionine decarboxylase
U77949	2.5	Cdc6-related protein (HsCDC6)
M95767	~2.5	di-N-acetylchitobiase
D83781	2.5	KIAA0197 gene

Table 11. cont'd...

X98534	2.5	vasodilator-stimulated phosphoprotein (VASP)
X53586	2.5	Integrin α 6*
D80001	2.4	KIAA0179 gene
L18960	2.4	protein synthesis factor (eIF-4C)
D23673	2.3	insulin receptor substrate-1 (IRS-1)
J02888	2.3	quinone oxidoreductase (NQO2)
D63487	2.3	KIAA0153 gene
U14603	2.3	protein-tyrosine phosphatase (HU-PP-1)
L41887	2.3	splicing factor, arginine/serine-rich 7 (SFRS7)
M92287	2.2	cyclin D3 (CCND3)
X61123	2.2	BTG1
AF002020	2.1	Niemann-Pick C disease (NPC1)
M95929	2.1	homeobox protein (PHOX1)
U32944	2.1	cytoplasmic dynein light chain 1 (hdlc1)
D79994	2.1	KIAA0172 gene (similar to ankyrin)
D89377	2	MSX-2
U90878	2	LIM domain protein CLP-36
U97105	2	N2A3 dihydropyrimidinase related protein-2
L40379	2	thyroid receptor interactor (TRIP10)
D00017	1.9	lipocortin II
J05459	1.9	glutathione transferase M3 (GSTM3)
D25328	1.9	platelet-type phosphofructokinase
M80254	1.9	cyclophilin isoform (hCyP3)
L42542	1.8	RLIP76 (ralA binding protein 1)
D42047	1.7	KIAA0089 similar to glycerol-3-phosphate dehydrogenase 1
M84349	1.7	transmembrane protein (CD59)
D43950	1.6	KIAA0098 T-COMPLEX PROTEIN 1 (TCP-1-EPSILON)
M15796	1.6	proliferating cell nuclear antigen (PCNA)

Table 12. Genes selectively downregulated by PR-B

Accession No.	Fold Decrease	Gene Name
U07225	~-4.3	P2U nucleotide receptor
M27492	~-3.4	interleukin 1 receptor mRNA
Y08682	-3.1	carnitine palmitoyltransferase I type I
U29091	~-2.9	selenium-binding protein (hSBP)
X79683	-2.6	beta2 laminin.
AB000220	-2.6	semaphorin E[1]
HG2197-HT2267	~-2.5	Collagen, Type Vii, Alpha 1
U65011	~-2.5	preferentially expressed antigen of melanoma (PRAME)
M18391	~-2.3	tyrosine kinase receptor (eph)
X71874	-1.9	proteasome-like subunit MECL-1

Table 13. Genes up or downregulated by progesterone via both PR-A and PR-B

Accession No.	Fold	Gene Name
U26726	~22.6	11-beta-hydroxysteroid dehydrogenase type 2
X51521	12.7	Ezrin*
U42031	9.4	progesterone receptor-associated FKBP54[1]
U70663	~7.5	zinc finger transcription factor EZF
U16799	6.1	Na,K-ATPase beta-1 subunit
M69043	4.2	MAD-3 (IkB-alpha)
X65614	3.6	calcium-binding protein S100P
D86962	2.9	Grb10
S81914	2.6	IEX-1=radiation-inducible immediate-early
U00115	2.4	bcl-6
M69225	~-3.5	bullous pemphigoid antigen (plakin family)
U90907	-3.2	clone 23907
J03241	~-3	transforming growth factor-beta 3 (TGF-beta3)
M92357	-2.1	tumor necrosis factor alpha-induced protein 2 (B94)

Table 14. Gene that is reciprocally regulated (upregulated by PR-B, downregulated by PR-A)

Accession No.	Fold	Gene Name
X53586	2.5	Integrin α 6*

Table 15. Group of genes for which the expression level is different depending on which isoform is present.

Accession No.	Fold	Gene Name
L13720	~23.1	growth arrest-specific protein (gas6)
M27436	~18.1	tissue factor gene
D79990	10.2	KIAA0168 Ras association (RalGDS/AF-6) domain family 2 (RASSF2)
U01120	~9.8	glucose-6-phosphatase
U37546	~7.2	IAP homolog C (MIHC)
D87953	6.8	RTP,DRG1,CAP43
M76180	~6.5	aromatic amino acid decarboxylase (ddc)
M77140	~6	pro-galanin
D50840	~5.6	ceramide glucosyltransferase
HG2743-HT2846	~5.1	Caldesmon 1 Non-Muscle
U76421	~4.7	dsRNA adenosine deaminase DRADA2b
U40572	4.6	beta2-syntrophin (SNT B2)
S69189	~4.5	peroxisomal acyl-coenzyme A oxidase
U44754	4.4	PSE-binding factor PTF gamma subunit
U02081	4.1	guanine nucleotide regulatory protein (NET1) oncogene
D16227	~4	BDP-1 (member of the recoverin family)
D17793	~4	3-alpha hydroxysteroid dehydrogenase type IIb
U83461	3.7	putative copper uptake protein (hCTR2)
M23254	3.6	Ca2+-activated neutral protease (CANP)
D15050	3.6	transcription factor AREB6
HG2167-HT2237	~3.5	Protein Kinase Ht31, Camp-Dependent
D10040	3.5	long-chain acyl-CoA synthetase
D31887	3.5	KIAA0062 gene
X60673	3.4	adenylate kinase 3
U45878	~3.3	inhibitor of apoptosis protein 1
L09229	3.3	long-chain acyl-coenzyme A synthetase (FACL1)
U09646	3.2	carnitine palmitoyltransferase II precursor (CPT1)
D31716	3.2	GC box bindig protein
M37400	3.1	cytosolic aspartate aminotransferase
X59834	3.1	glutamine synthase
D78335	3.1	uridine monophosphate kinase (UMPK)
U41387	3	RNA helicase II/Gu)
U07919	3	aldehyde dehydrogenase 6
M69013	2.9	guanine nucleotide-binding regulatory protein (G-y-alpha)
HG2530-HT2626	2.9	Adenylyl Cyclase-Associated Protein 2
U79288	2.8	clone 23682
D10704	2.6	choline kinase
Y08134	2.6	ASM-like phosphodiesterase 3b
U33632	2.6	two P-domain K+ channel TWIK-1
M21154	2.5	S-adenosylmethionine decarboxylase
U77949	2.5	Cdc6-related protein (HsCDC6)
M95767	~2.5	di-N-acetylchitobiase
D83781	2.5	KIAA0197 gene
X98534	2.5	vasodilator-stimulated phosphoprotein (VASP)
D80001	2.4	KIAA0179 gene
L18960	2.4	protein synthesis factor (eIF-4C)
D23673	2.3	insulin receptor substrate-1 (IRS-1)
J02888	2.3	quinone oxidoreductase (NQO2)

Table 15. Cont'd...

D63487	2.3	KIAA0153 gene
U14603	2.3	protein-tyrosine phosphatase (HU-PP-1)
L41887	2.3	splicing factor, arginine/serine-rich 7 (SFRS7)
M92287	2.2	cyclin D3 (CCND3)
X61123	2.2	BTG1
M95929	2.1	homeobox protein (PHOX1)
U32944	2.1	cytoplasmic dynein light chain 1 (hdlc1)
D79994	2.1	KIAA0172 gene (similar to ankyrin)
D89377	2	MSX-2
U90878	2	LIM domain protein CLP-36
U97105	2	N2A3 dihydropyrimidinase related protein-2
L40379	2	thyroid receptor interactor (TRIP10)
J05459	1.9	glutathione transferase M3 (GSTM3)
L42542	1.8	RLIP76 (ralA binding protein 1)
D42047	1.7	KIAA0089 similar to glycerol-3-phosphate dehydrogenase 1
M84349	1.7	transmembrane protein (CD59)
D43950	1.6	KIAA0098 T-COMPLEX PROTEIN 1 (TCP-1-EPSILON)
M15796	1.6	proliferating cell nuclear antigen (PCNA)
U07225	~-4.3	P2U nucleotide receptor
M27492	~-3.4	interleukin 1 receptor mRNA
Y08682	-3.1	carnitine palmitoyltransferase I type I
U29091	~-2.9	selenium-binding protein (hSBP)
X79683	-2.6	beta2 laminin.
AB000220	-2.6	semaphorin E
HG2197-HT2267	~-2.5	Collagen, Type Vii, Alpha 1
U65011	~-2.5	preferentially expressed antigen of melanoma (PRAME)
M18391	~-2.3	tyrosine kinase receptor (eph)
X71874	-1.9	proteasome-like subunit MECL-1
L43821	4.7	enhancer of filamentation (HEF1)
L38487	2.3	estrogen receptor-related protein (hERRa1)
D25539	~8	KIAA0040 gene
HG4069-HT4339	~-7.4	Monocyte Chemotactic Protein 1

Table 16. Genes encoding products involved in breast cancer or mammary gland development*.

Accession no.	Fold	Gene Name
L13720	~23.1	growth arrest-specific protein (gas6)
M27436	~18.1	tissue factor gene
M83667	6.4	NF-IL6-beta (C/EBPbeta)*
M68516	~6.2	PCI gene (plasminogen activator inhibitor)
U43185	~6.1	Stat5A*
X65614	3.6	calcium-binding protein S100P
X53586	2.5	**Integrin α 6***
D89377	2	MSX-2*
D00017	1.9	lipocortin II (calpactin I)
U29091	~-2.9	selenium-binding protein (hSBP)
M69225	~-3.5	bullous pemphigoid antigen (plakin family)

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Table 17. Genes regulated by progesterone organized by primary function of gene product.

Accession no.	Fold	Gene Name	Regulation Pattern
Transcription factors			
U70663	~7.5	zinc finger transcription factor EZF	Up by Both
M83667	6.4	NF-IL6 (C/EBPbeta)	Up by PR-B
U43185	~6.1	Stat5A	Up by PR-B
D15050	3.6	transcription factor AREB6	Up by PR-B
D31716	3.2	GC box bindig protein	Up by PR-B
U00115	2.4	bcl-6	Up by Both
U44754	4.4	PSE-binding factor PTF gamma subunit	Up by PR-B
M95929	2.1	homeobox protein (PHOX1)	Up by PR-B
S81914	2.6	IEX-1=radiation-inducible DIF2	Up by Both
D89377	2	MSX-2	Up by PR-B
Z50781	2.5	delta sleep inducing peptide (higly related to TSC-22)	Up by PR-A
L38487	2.3	estrogen receptor-related protein (hERRa1)	Up by PR-A
Cell adhesion or cytoskeleton interaction			
HG2743-HT2846	~5.1	Caldesmon 1 Non-Muscle	Up by PR-B
L43821	4.7	enhancer of filamentation (HEF1)	Up by PR-A
U40572	4.6	beta2-syntrophin (SNT B2)	Up by PR-B
X98534	2.5	vasodilator-stimulated phosphoprotein (VASP)	Up by PR-B
U32944	2.1	cytoplasmic dynein light chain 1 (hdlc1)	Up by PR-B
U90878	2	LIM domain protein CLP-36	Up by PR-B
X79683	-2.6	beta2 laminin.	Down by PR-B
L43821	4.7	enhancer of filamentation (HEF1)	Up by PR-A
Calcium binding proteins			
D16227	~4	BDP-1 (member of the recoverin family)	Up by PR-B
X65614	3.6	calcium-binding protein S100P	Up by Both
D00017	1.9	lipocortin II (calpactin I)	Up by PR-B
Cholesterol or steroid metabolism and trafficking			
U26726	~22.6	11-beta-hydroxysteroid dehydrogenase type 2	Up by Both
D17793	~4	3-alpha hydroxysteroid dehydrogenase type IIb	Up by PR-B
AF002020	2.1	Niemann-Pick C disease (NPC1)	Up by PR-B

Table 17. cont'd...

Fatty acid/lipid metabolism			
M76180	~6.5	aromatic amino acid decarboxylase (ddc)	Up by PR-B
D50840	~5.6	ceramide glucosyltransferase (phospholipid synthesis)	Up by PR-B
S69189	~4.5	peroxisomal acyl-coenzyme A oxidase	Up by PR-B
X52730	4.4	phenylethanolamine n-methyltransferase (PNMT)	Up by PR-B
L09229	3.3	long-chain acyl-coenzyme A synthetase (FACL1)	Up by PR-B
U09646	3.2	carnitine palmitoyltransferase II precursor (CPT1)	Up by PR-B
X59834	3.1	glutamine synthase	Up by PR-B
D78335	3.1	uridine monophosphate kinase (UMPK)	Up by PR-B
Y08134	2.6	ASM-like phosphodiesterase 3b	Up by PR-B
J02888	2.3	quinone oxidoreductase (NQO2)	Up by PR-B
Y08682	-3.1	carnitine palmitoyltransferase I type I	down by PR-B
Nucleotide or amino acid metabolism			
M37400	3.1	cytosolic aspartate aminotransferase (amino acid metabolism)	Up by PR-B
U97105	2	N2A3 dihydropyrimidinase related protein-2	Up by PR-B
U07225	~-4.3	P2U nucleotide receptor	down by PR-B
General metabolic/synthetic			
U01120	~9.8	glucose-6-phosphatase (gluconeogenesis)	Up by PR-B
U07919	3	aldehyde dehydrogenase 6 (alcohol metabolism)	Up by PR-B
M21154	2.5	S-adenosylmethionine decarboxylase (polyamine biosynthesis)	Up by PR-B
M95767	~2.5	di-N-acetylchitobiase (glycoprotein synthesis)	Up by PR-B
D42047	1.7	KIAA0089 gene (similar to glycerol-3-phosphate dehydrogenase 1)	Up by PR-B
J05459	1.9	glutathione transferase M3 (GSTM3)	Up by PR-B
D25328	1.9	platelet-type phosphofructokinase	Up by PR-B
U29091	~-2.9	selenium-binding protein (hSBP)	down by PR-B
DNA-replication/transcription/translationand protein processing			
U76421	~4.7	dsRNA adenosine deaminase DRADA2b	Up by PR-B
U41387	3	RNA helicase II/Gu	Up by PR-B
L18960	2.4	protein synthesis factor (eIF-4C)	Up by PR-B
L41887	2.3	splicing factor, arginine/serine-rich 7 (SFRS7)	Up by PR-B

Table 17. cont'd...

U77949	2.5	Cdc6-related protein (HsCDC6)	Up by PR-B
X71874	-1.9	proteasome-like subunit MECL-1	Down by PR-B
Secreted molecules			
L13720	~23.1	growth arrest-specific protein (gas6)	Up by PR-B
M27436	~18.1	tissue factor gene	Up by PR-B
M68516	~6.2	PCI gene (plasminogen activator inhibitor 3)	Up by PR-B
M77140	~6	pro-galanin	Up by PR-B
M23254	3.6	Ca2+-activated neutral protease (CANP)	Up by PR-B
AB000220	-2.6	semaphorin E	Down by PR-B
Signal transduction			
D79990	10.2	KIAA0168 Ras association (RalGDS/AF-6) domain family 2 (RASSF2)	
M69043	4.2	MAD-3 encoding IkB-alpha	Up by Both
U02081	4.1	guanine nucleotide regulatory protein (NET1) oncogene	Up by PR-B
HG2167-HT2237	~3.5	Protein Kinase Ht31, cAMP-Dependent	Up by PR-B
X60673	3.4	adenylate kinase 3	Up by PR-B
HG2530-HT2626	2.9	Adenylyl Cyclase-Associated Protein 2	Up by PR-B
D86962	2.9	Grb10	Up by Both
M69013	2.9	guanine nucleotide-binding regulatory protein (G-y-alpha)	Up by PR-B
D10704	2.6	choline kinase	Up by PR-B
U14603	2.3	protein-tyrosine phosphatase (HU-PP-1)	Up by PR-B
L40379	2	thyroid receptor interactor (TRIP10)	Up by PR-B
M18391	~-2.3	tyrosine kinase receptor (eph)	Down by PR-B
U44103_at	-2.8	small GTP binding protein Rab9	Down by PR-A
Cytokines/Cytokine Receptors and Chemokines			
M27492	~-3.4	interleukin 1 receptor mRNA	Down by PR-B
J03241	~-3	transforming growth factor-beta 3 (TGF-beta3)	Down by Both
HG4069-HT4339_s_at	~-7.4	Monocyte Chemotactic Protein 1	Down by PR-A

Table 17. cont'd...

Membrane bound molecules			
U16799	6.1	Na,K-ATPase beta-1 subunit	Up by Both
U83461	3.7	putative copper uptake protein (hCTR2)	Up by PR-B
U33632	2.6	two P-domain K+ channel TWIK-1	Up by PR-B
M84349	1.7	transmembrane protein (CD59)	Up by PR-B
M69225	~-3.5	bullous pemphigoid antigen (plakin family)	Down by Both
U65011	~-2.5	preferentially expressed antigen of melanoma (PRAME)	Down by PR-B
Chaperones/Protein folding			
U42031	9.4	progesterone receptor-associated FKBP54	Up by Both
M80254	1.9	cyclophilin isoform (hCyP3)	Up by PR-B
Apoptosis			
U37546	~7.2	IAP homolog C (bindsTNFreceptor-associated factors)	Up by PR-B
U45878	~3.3	inhibitor of apoptosis protein 1 mRNA	Up by PR-B
Cell cycle			
D87953	6.8	RTP	Up by PR-B
M92287	2.2	cyclin D3 (CCND3)	Up by PR-B
M15796	1.6	proliferating cell nuclear antigen (PCNA)	Up by PR-B
X61123	2.2	BTG1	Up by PR-B
Unknown Function			
D25539	~8	KIAA0040 gene	Up by PR-B
D31887	3.5	KIAA0062 gene	Up by PR-B
U79288	2.8	clone 23682	Up by PR-B
D83781	2.5	KIAA0197 gene	Up by PR-B
D80001	2.4	KIAA0179 gene	Up by PR-B
D63487	2.3	KIAA0153 gene	Up by PR-B
D79994	2.1	KIAA0172 gene (similar to ankyrin)	Up by PR-B
M92357	-2.1	tumor necrosis factor, alpha-induced protein 2 B94	Down by PR-B
U90907	-2.1	clone 23907 (similar to mouse p55PIK)	Down by Both

Table18. Transcripts regulated in T47D-YB cells after 6hrs progesterone treatment

Accession no.	Fold Increase	Gene Name
L13720	~23.1	growth arrest-specific protein (gas6)
U26726	~22.6	11-beta-hydroxysteroid dehydrogenase type 2
M27436	~18.1	tissue factor gene
D79990	10.2	KIAA0168 Ras association (RalGDS/AF-6) domain family 2 (RASSF2)
U01120	~9.8	glucose-6-phosphatase
U42031	9.4	progesterone receptor-associated FKBP54*
D25539	~8	KIAA0040 gene
U70663	~7.5	zinc finger transcription factor EZF
U37546	~7.2	IAP homolog C (MIHC)
D87953	6.8	RTP,DRG1,CAP43
M76180	~6.5	aromatic amino acid decarboxylase (ddc)
M83667	6.4	NF-IL6 (C/EBPbeta)
M68516	~6.2	PCI gene (plasminogen activator inhibitor 3)
U43185	~6.1	Stat5A
U16799	6.1	Na,K-ATPase beta-1 subunit
M77140	~6	pro-galanin
D50840	~5.6	ceramide glucosyltransferase
HG2743-HT2846	~5.1	Caldesmon 1 Non-Muscle
U76421	~4.7	dsRNA adenosine deaminase DRADA2b
U40572	4.6	beta2-syntrophin (SNT B2)
S69189	~4.5	peroxisomal acyl-coenzyme A oxidase
U44754	4.4	PSE-binding factor PTF gamma subunit
X52730	4.4	phenylethanolamine n-methyltransferase (PNMT)
M69043	4.2	MAD-3 (IkB-alpha)
U02081	4.1	guanine nucleotide regulatory protein (NET1) oncogene*
D16227	~4	BDP-1 (member of the recoverin family)
D17793	~4	3-alpha hydroxysteroid dehydrogenase type IIb
U83461	3.7	putative copper uptake protein (hCTR2)
X65614	3.6	calcium-binding protein S100P
M23254	3.6	Ca2+-activated neutral protease (CANP)
D15050	3.6	transcription factor AREB6
HG2167-HT2237	~3.5	Protein Kinase Ht31, Camp-Dependent
D10040	3.5	long-chain acyl-CoA synthetase
D31887	3.5	KIAA0062 gene
X60673	3.4	adenylate kinase 3
U45878	~3.3	inhibitor of apoptosis protein 1
L09229	3.3	long-chain acyl-coenzyme A synthetase (FACL1)
U09646	3.2	carnitine palmitoyltransferase II precursor (CPT1)
D31716	3.2	GC box bindig protein
M37400	3.1	cytosolic aspartate aminotransferase
X59834	3.1	glutamine synthase
D78335	3.1	uridine monophosphate kinase (UMPK)
U41387	3	RNA helicase II/Gu)
U07919	3	aldehyde dehydrogenase 6
D86962	2.9	Grb10
M69013	2.9	guanine nucleotide-binding regulatory protein (G-y-alpha)*
HG2530-HT2626	2.9	Adenylyl Cyclase-Associated Protein 2
U79288	2.8	clone 23682
D10704	2.6	choline kinase
Y08134	2.6	ASM-like phosphodiesterase 3b
U33632	2.6	two P-domain K+ channel TWIK-1
S81914	2.6	IEX-1=radiation-inducible immediate-early
M21154	2.5	S-adenosylmethionine decarboxylase

Table 18. cont'd...

U77949	2.5	Cdc6-related protein (HsCDC6)
M95767	~2.5	di-N-acetylchitobiase
D83781	2.5	KIAA0197 gene
X98534	2.5	vasodilator-stimulated phosphoprotein (VASP)
D80001	2.4	KIAA0179 gene
L18960	2.4	protein synthesis factor (eIF-4C)
U00115	2.4	bcl-6
J02888	2.3	quinone oxidoreductase (NQO2)
D63487	2.3	KIAA0153 gene
U14603	2.3	protein-tyrosine phosphatase (HU-PP-1)
L41887	2.3	splicing factor, arginine/serine-rich 7 (SFRS7)
M92287	2.2	cyclin D3 (CCND3)
X61123	2.2	BTG1
AF002020	2.1	Niemann-Pick C disease (NPC1)
M95929	2.1	homeobox protein (PHOX1)
U32944	2.1	cytoplasmic dynein light chain 1 (hdlc1)
D79994	2.1	KIAA0172 gene (similar to ankyrin)
D89377	2	MSX-2
U90878	2	LIM domain protein CLP-36
U97105	2	N2A3 dihydropyrimidinase related protein-2
L40379	2	thyroid receptor interactor (TRIP10)
D00017	1.9	lipocortin II
J05459	1.9	glutathione transferase M3 (GSTM3)
D25328	1.9	platelet-type phosphofructokinase
M80254	1.9	cyclophilin isoform (hCyP3)
L42542	1.8	RLIP76 (ralA binding protein 1)
D42047	1.7	KIAA0089 similar to glycerol-3-phosphate dehydrogenase 1
M84349	1.7	transmembrane protein (CD59)
D43950	1.6	KIAA0098 T-COMPLEX PROTEIN 1 (TCP-1-EPSILON)
M15796	1.6	proliferating cell nuclear antigen (PCNA)

Accession no.	Fold Decrease	Gene Name
U07225	~-4.3	P2U nucleotide receptor
M69225	~-3.5	bullous pemphigoid antigen (plakin family)
M27492	~-3.4	interleukin 1 receptor mRNA
U90907	-3.2	clone 23907
Y08682	-3.1	carnitine palmitoyltransferase I type I
J03241	~-3	transforming growth factor-beta 3 (TGF-beta3)
U29091	~-2.9	selenium-binding protein (hSBP)
X79683	-2.6	beta2 laminin.
AB000220	-2.6	semaphorin E*
HG2197-HT2267	~-2.5	Collagen, Type Vii, Alpha 1
U65011	~-2.5	preferentially expressed antigen of melanoma (PRAME)
M18391	~-2.3	tyrosine kinase receptor (eph)
M92357	-2.1	tumor necrosis factor, alpha-induced protein 2 B94
X71874	-1.9	proteasome-like subunit MECL-1

Table 19. Transcripts regulated in T47D-YA cells after 6hrs progesterone treatment

Accession no.	Fold Increase	Gene Name
U26726	6.5	11-beta-hydroxysteroid dehydrogenase type 2
L43821	4.7	**enhancer of filamentation (HEF1)**
U70663	~7.5	zinc finger transcription factor EZF
U16799	3.9	Na,K-ATPase beta-1 subunit
U42031	3.3	progesterone receptor-associated FKBP54
Z50781	2.5	**delta sleep inducing peptide (higly related to TSC-22)**
L38487	2.3	**estrogen receptor-related protein (hERRa1)**
U00115	2.3	bcl-6
X65614	2.2	calcium-binding protein S100P
S81914	2.1	IEX-1=radiation-inducible immediate-early
M69043	2.0	MAD-3 mRNA (IkB-alpha)
D86962	2.0	Grb10

Accession no.	Fold Decrease	Gene Name
HG4069-HT4339	~-7.4	**Monocyte Chemotactic Protein 1**
M69225	~-4.3	bullous pemphigoid antigen (BPAG1)
J03241	-3.3	transforming growth factor-beta 3 (TGF-beta3)
M92357	-3.0	tumor necrosis factor, alpha-induced protein 2 B94
U44103	-2.8	**small GTP binding protein Rab9**
U90907	-2.1	clone 23907

While various embodiments of the present invention have been described in detail, it is apparent that modifications and adaptations of those embodiments will occur to those skilled in the art. It is to be expressly understood, however, that such modifications and adaptations are within the scope of the present invention, as set forth in the following claims.